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GenCore version 5.1.3
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OM protein - protein search, using sw model

6, 2003, 12:46:55; Search time 28.5758 Seconds (without alignments) 573.557 Million cell updates/sec January Run on:

US-09-155-739-11

655 1 QVQLVQSGAEVKKPGASVKV.....NYGVYAMDYWGQGTLVTVSS 123 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

908470

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					COLUMNICO	
		æ				
Result	groop	Query	Query	ä	£	Description
	2000	11000		3	4	
П	655	100.0	123	16	AAR81323	Humanized VLA-4 an
7	655			16	AAR81333	Human VLA-4 reshap
m	655			18	AAW22428	Humanised alpha-4
4	648			18	AAW22413	Humanised alpha-4
2	552			16	AAR81330	Mouse anti-VLA-4 a
9	544			16	AAR81327	Mouse VLA-4 antibo
7	544			18	AAW22410	Alpha-4 integrin m
80	523.5			19	AAW44124	Heavy chain variab
6	523.5	79.9	120	23	AAU79034	Humanised antibody
10	523.5			22	AAB30693	A fusion of single

New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.

Saldanha J;

Leger OJ,

Bendig MM, Jones TS, WPI; 1995-269276/35

Human/murine chime Chimaeric human/mu Human ONS-M21 anti Chimaeric human/mu Humanized VLA-4 an Humanized alpha-4 A heavy chain vari Monoclonal alpha-4 A heavy chain vari Monse and human ch Human monoclonal a hILZR AD H Chain V Humanised ATR-5 H	ATR-5 ATR-5 ATR-5 ATR-5 anti-C human
AAR76681 AAR04396 AAR04396 AAR04324 AAR81325 AAR81324 AAR81324 AAR81324 AAR81324 AAR81324 AAR81396 AAR37611 AAR37611 AAR37611 AAR37611 AAR37611 AAR3761 AAR3761 AAR3761 AAR3761 AAR37718 AAR37718 AAR37718 AAR37718 AAR37718 AAR37718 AAR37718 AAR37718 AAR37718 AAR37718 AAR37718 AAR37718 AAR37718 AAR37718 AAR37718 AAR37718 AAR37718	74 0 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3
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523 523 523 523 523 515 515 515 515 507 507 508 508 503 501 503 503 601 503 603 603 603 603 603 603 603 603 603 6	489.5 489 489 487.5 487.5
	044444 0012648

ALIGNMENTS

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Humanized antibody; leukocyte adhesion molecule; {\it VLA-4}; therapeutic; antibody engineering.
                                                               Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
                AAR81323 standard; Protein; 123 AA.
                                                                                                                                                                                      (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                      95WO-US01219.
                                                                                                                                                                     94US-0186269
                                               02-APR-1996 (first entry)
                                                                                                        Mus musculus.
                                                                                                                                                      25-JAN-1995;
                                                                                                                                                                     25-JAN-1994;
                                                                                                                       WO9519790-A1
                                                                                                                                      27-JUL-1995.
                                AAR81323;
RESULT 1
         AAR81323
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                       The sequence encodes the mouse antibody 21.6 heavy chain variable region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned CDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ9985-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids LA5, LA9 LAS and LG9 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmids encoding the chimmeric antibodies are transfected into COS cells. The humanized antibodies can be used
                                                                                                                                                                                          1.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used for inhibiting adhesion of a leukocyte to an endothelial cell and for tracating inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DPKFQGRVTITADISASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human VLA-4 reshaped antibody 21.6 light heavy variable region.
                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 655; DB 16; Length 123; 100.0%; Pred. No. 6.6e-53; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "complementarity determining region 1"
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132..142
/note="framework region 4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR81333 standard; Protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
Claim 11; Page 69; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.
Matches 123; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody engineering.
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                                                                                                                                                                                                                                                                                                                                              Sednence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple solerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA 4, for affinity purification or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWYRQAPGQRLEWMGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                            chain variable region against leukocyte adhesion molecule VLA-4.
Cloned cDNA sequences of mouse 21.6 VH (Ang99802) and VL (Ang099889)
regions are linked to human constant regions in the construction
of a humanized antibody against VLA-4. The 5' and 3' ends of the
mouse cDNAs are modified using PCR primers (Ang99895-98) and then
subcloned into mammalian cell expression vectors containing human
kappa or gamma-1 constant regions. In the humanized heavy chain,
amino acids 127, 143, 143, 143, 140, 141 and 171 in the human HC VR
position of the mouse 21 6 19 H chain. Plasmids encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents the human reshaped antibody 21.6 heavy
                                                                                                                                                                                                                                                                                         New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised alpha-4 integrin antibody 21.6 VL version Ha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 655; DB 16;
100.0%; Pred. No. 7.8e-53;
iive 0; Mismatches 0;
                                                                                                                                                                                               Leger OJ, Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 11; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW22428 standard; Protein; 142 AA.
                                                                                                                                                       (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                  94US-0186269.
                                                                           95WO-US01219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 123; Conservative
                                                                                                                                                                                             Bendig MM, Jones TS,
                                                                                                                                                                                                                                                                                                                                    inflammatory disease.
                                                                                                                                                                                                                                WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 AA;
                                                                                                                                                                                                                                                      N-PSDB; AAQ99894.
WO9519790-A1.
                                                                             25-JAN-1995;
                                                                                                                25-JAN-1994;
                                      27-JUL-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 VSS 123
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This polypeptide, designated Ha, comprises the heavy chain variable region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also AMM22413) It is composed of complementarity determining regions from the VH region (see AMM22410) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human 21/28 CL framework. It can be expressed in mammallan host cells following PCR amplification and mutagenesis of appropriate mouse and human DNA sequences. The humanised 21.6 VH and a humanised 21.6 VL (see AAM22412) can be used to produce a claimed humanised 21.6 antibody that is useful in the manufacture of a medicament for treating asthma, atherosclerosis, canthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psorlasis, myocardial ischemia, and acute leukocyte mediated lung injury. The humanised equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR3
/note= "21.6 complementarity determining region 3"
                                                                                                                                                                                                                                                          /note= "21.6 complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                              "21.6 complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= FR4
/note= "21/28'CL framework region 4"
                                                                                                                                                                                                                /note= "21/28'CL framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                      "21/28'CL framework region 3"
                                                                                                                                                                                                                                                                                                    "21/28'CL framework region 2"
atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                                                          /label= Mat_protein
/note= "VH version Ha (Claim 25)"
                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Fig 11; 107pp; English
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                                                                                                                   ...19
'label= Leader
                                                                                                                                                                                                                                                                                                                               /label= CDR2
                                                                                                                                                                                                                                            /label= CDR1
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                                                                                                                                                                                                                                                                                   /label- FR2
                                                                                                                                                                                                                                                                                                                                                                          /label= FR3
                                                                                                                                                                                                    /label- FR1
                                                                                                                                                                                                                                                                                                                                                                                                       .131
                                                                                                                                                                                                                                                                                                                                                                                                                                                 .142
                                                                                                                                                                                                                                                                                                       /note=
                                         Chimeric Mus musculus;
Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-297879/27.
                                                                    Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAY-1997
                                                                                                             Peptide
                                                                                                                                           Protein
                                                                                                                                                                                     Region
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Sequence

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Gaps
                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                             20 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWYRQAPGQRLEWMGRIDPANGYIKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "21.6 complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "21.6 complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "21.6 complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "21/28'CL Arg-72 is substd. by Ala of mouse 21.6 VL, important in supporting the CDR2
                                                                                                                                                                                                                                                                                                                                    Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psorlaais; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "21/28'CL residues 27-30 are replaced by those of MAD 21.6, involved in antigen
                         ö
  Length 142;
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "21/28'CL framework region 1" 17..30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113..123
|Jabel= FR4
|note= "21/28'CL framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "21/28'CL framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note- "21/28'CL framework region 2"
100.0%; Score 655; DB 18; ilarity 100.0%; Pred. No. 7.8e-53; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                              Humanised alpha-4 integrin antibody 21.6 VH Ha.
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                                                                                                                                                                                                                                     AAW22413 standard; Protein; 123 AA.
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/label= CDR2
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/label= FR3
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                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric Mus musculus;
Chimeric Homo sapiens;
Chimeric synthetic.
 Query Match
Best Local Similarity
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                                                                                                                                                  121 VSS 123
                                                                                                                                                                          140 VSS 142
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                        Matches 123;
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1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-269276/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanized antibody; leukocyte adhesion molecule; {\it VLA-4}; therapeutic; antibody engineering.
                                                                                                                                                                                                                                                                                                                            metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukcoyte mediated lung injury. The antibody for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                              Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
98.9%; Score 648; DB 18; Length 123;
Best Local Similarity 99.2%; Pred. No. 2.9e-52;
Matches 122; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
                                                                                 Saldanha J, Yednock TA;
                                                                                                                                          asthma, atherosclerosis, AIDS, dementia, etc.
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                                                                                   Leger OJ,
                                                         (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                               Claim 25; Fig 7; 107pp; English.
             96WO-US18807
                                   95us-0561521
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/label= FR1
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                                                                                 Jones ST,
                                                                                                       WPI; 1997-297879/27
                                                                                                                                                                                                                                                                                                                                                                                                                        123 AA;
             21-NOV-1996;
                                  21-NOV-1995;
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                                                                                 Bendig MM,
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The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain variable region (without signal sequence). Cloned cDNA CDR sequences of mouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the REI antibody for the 140th chain and antibody against VLA-4. The 5' and 3' ends of the mususe cDNAs are modified using PCR primers (See Ang09895-98) and then subcloned into constant regions. In the humanized light chain, amino acids LA5, LA9, CCS and L69 in the human kappa LCVR framework are replaced by the amino constant regions. In the humanized light chain, amino acids LA5, LA9, CCS acid present in the equivalent position of the mouse 21.6 Ig light chain. Plasmids encoding the chimeric antibodies are transfected into COS collain. Plasmids antibodies can be used to inhibit adhesion of a cleukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used to see used in the treatment of stroke, cused for detecting VLA-4, for affinity purification or for generating entity and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                            /label- CDR2
/note- "mouse heavy chain variable complementarity
determining region 2"
                                                                                                                                                        /note= "mouse heavy chain variable complementarity
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                                                                                                                                                                                                                                                                                                                 /note= "mouse heavy chain variable framework region 2"
'note= "mouse heavy chain variable framework
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                                             region 1"
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                                                                                                               /label= CDR1
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                                                region directed against leukocyte adhesion molecule VLA-4. Cloned CDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse CDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1
The sequence represents the mouse antibody 21.6 heavy chain variable
                                                                                                                                                                                                                                                                 flumanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                   DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New humanised antibodies against VIA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                  "complementarity determining region 1"
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                                                                                                                                                                                                                                         Mouse VLA-4 antibody 21.6 light heavy variable region.
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                                                                                                                                                                                                                                                                                                                                                  "signal peptide"
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                                                                                                                                                                   AAR81327 standard; Protein; 140 AA.
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                                                                                                                                                                                                                                                                             antibody engineering.
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N-PSDB; AAQ99892.
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                                                                                 VSS 123
                                                                                                        VSS 123
                                                                                                                                                                                                                                                                                                     Aus musculus
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constant regions. In the humanized heavy chain, amino acids H27, H28, H29, H30, H44 and H71 in the human HC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig H chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They meningtis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis;
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                                                                                                                                                                                                Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                             83.1%; Score 544; DB 16;
82.6%; Pred. No. 1.3e-42;
ive 11; Mismatches 10;
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/label= FR3
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/label- FR4
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/label= CDR1
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/label= C
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les 100; Conservative
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                                                                                                                                                                    140 AA;
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                                                                                                                                                                                                                                                                                                                                                                              This polypeptide comprises the heavy chain variable region (VH) of mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VH can be incorporated into a human 21/28'CL framework to produce a claimed humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6 rantibody that is used in the manufacture of a medicament for treating a disease selected from asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin generating idiotypic antibodies. The humanised antibodies of the inventon have a half-life in the human circulation essentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heavy chain; variable region; murine; mouse; human; cancer antigen;
antibody; humanised; NR-LU-13; NRX451; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heavy chain variable region of humanised NR-LU-13 antibody NRX451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                 Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 140;
                                                                                                                                                                                                            Leger OJ, Saldanha J, Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.1%; Score 544; DB 18;
82.6%; Pred. No. 1.3e-42;
tive 11; Mismatches 10;
/note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 69-70; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW44124 standard; Protein; 120 AA.
                                                                                                                                                                           (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                          95US-0561521.
                                                                                                       96WO-US18807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 100; Conservative
                                                                                                                                                                                                          Bendig MM, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                             WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 AA;
                                                                                                                                                                                                                                                                 N-PSDB; AAT74760.
                                 WO9718838-A1
                                                                                                     21-NOV-1996;
                                                                                                                                        21-NOV-1995;
                                                                    29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 V 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 V 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW44124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
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61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              novel humanised Ab (hAb) binds the antigen bound by NR-LU-13. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised antibody binds same human cancer antigen as antibody NR-LU-13 - useful for pre-targeting methods, conventional antibody therapy and immunodiagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the heavy chain variable region of the humanised murine anti-human cancer antigen antibody (Ab) NR-LU-13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hAb, specifically NRX451, or its conjugates can be used for the manufacture of a diagnostic or medicament for cancer diagnosis or treatment. The hAb has reduced immunogenicity and toxicity in humans, but retains the ability to bind the NR-LU-13 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 19; Length 120;
                                                                     /note= "complementarity determining region 2" 99..109
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pedersen JT;
                                                                                                                                               /note= "complementarity determining region 3"
                                          /note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanised antibody NRX451 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; NR-LU-13; humanised antibody; NX451; cancer; cytostatic; heavy chain variable region; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 79.9%; Score 523.5; DB 19; Best Local Similarity 82.9%; Pred. No. 8.3e-41; Matches 102; Conservative 8; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mallet RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hylarides MD,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU79034 standard; Protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 4; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Graves SS, Henry AH, Hylaride
Rees AR, Renojm, Searle SMJ;
                                                                                                                                                                                                                                                                                                    97WO-US10074
                                                                                                                                                                                                                                                                                                                                                       960S-0660362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-042124/04.
                                                                                                                                                                                                                                                                                                                                                                                                         (NEOR-) NEORX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 AA;
                                                                                                                                                                                               W09746589-A2.
                                                                                                                                                                                                                                                                                                    06-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 VSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 VSS 123
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                                                                                                                                                                                                                                                  11-DEC-1997
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                                                                                                                                                                                                                                                                                The invention relates to the humanised antibody NRX 451 (or an antigenbinding fragment), in which the murine parent antibody is ATCC CRL-12360 (also known as NU-LU-13 which targets a 40 kilodalton glycoprotein expressed by many carcinomas) and which comprises the light chain variable region appearing as AAU79033 and the heavy chain variable region appearing as AAU79033 and the heavy chain variable region appearing as AAU79033 and the heavy chain variable region appearing as AAU79033 and the heavy chain variable region appearing as AAU79033 and the nearly man is a milbody is a humanised antibody derived from NR-LU-13 amples. The antibody is a humanised antibody derived from NR-LU-13 antigen. The antibody glycosylation or its N-linked glycosylation or its N-linked glycosylation are specially. The present sequence represents the heavy chain variable region of humanised antibody of the invention, NRX451.
                                                                                                                                                                                                              Humanised antibody NRX-451, which is derived from ATCC CRL-12360, but which has reduced immunogenicity or toxicity, useful for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DLSFQGRVTITADTSINTAYMELSSLRSDDTAVYYCSREVL---TGTWSLDYWGQGTLVT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DPKFQGRVTITADISASTAYMELSSLRSEDIAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYMHWVRQAPGQGLQWMGRIDPANGNTKC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 23; Length 120;
                                                                                                                                                       Searle SMJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.9%; Score 523.5; DB 23; Length
82.9%; Pred. No. 8.3e-41;
cive 8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptavidin; tumour cell; cancer; adenocarcinoma; hematological malignancy; huNR-LU-10; EGP40; EPCAM
                                                                                                                                                       Hylarides MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A fusion of single chain antibody/streptavidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB30693 standard; Protein; 431 AA
                                                                                                                                                     Reno JM, Mallett RW,
Pedersen JT, Rees AR;
                                                                                                                                                                                                                                                             Claim 1; Fig 4; 53pp; English.
                                                                                97US-0871488.
                                                                                                       96US-0660362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces avidinil.
                                                                                                                                                       Graves SS, Reno JM,
                                                                                                                                                                                        WPI; 2002-314754/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                       treating cancers -
                                                                                                                              (NEOR-) NEORX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 AA;
Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 VSS 120
                                 US6358710-B1
                                                                                                       17-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-APR-2001
                                                        19-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                   Henry AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB30693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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The present sequence encodes a fusion of the single chain antibody bunkr.LD-10 and streptavidin. The antibody binds the antigen EGP40 or EPCAM. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin or its functional variant operatively linked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a first nucleic acid operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a vector construct comprises a first nucleic acid operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a vector construct comprises a first nucleic acid encoding at least comprises a first nucleic acid encoding at least comprise and in streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer, e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               presence or absence of, or treating, a target site within a mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reno JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with cancer, e.g. adenocarcinomas -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 OVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 DLSFQGRVIITADTSINTAYMELSSLRSDDTAVYYCSREVL---TGTWSLDYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sanderson JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human/murine chimeric antibody HEF-RVL-M21g(gamma)1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schultz JE, Lin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR76681 standard; Protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 10; 100pp; English
                                                                                                                                                                                                                           05-JUN-2000; 2000WO-US15595.
                                                                                                                                                                                                                                                                                                     99US-0137900.
99US-0168976.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goshorn SC, Graves SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-091213/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                           (NEOR-) NEORX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAC86562
                                                                     WO200075333-A1.
Homo sapiens.
                                                                                                                                                                                                                                                                                                         07-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                             03-DEC-1999;
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                                                                                                                                                  14-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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The present sequence is a fragment of the chimaeric human/murine monoclonal antibody (MAD) ONS-M21. The MAD was prepd. by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAD, with human light and heavy constant region sequences, respectively to produce chimaeric human/murine light and heavy and light chain DNA mols. A recombinant vector of for the expression of the heavy and light chain DNA mols. was prepd., and used to transform a host cell. The host cell was then cultured, and the expression prods. of the heavy and light chain CNA mols. sepd. and connected with a peptide linker to produce a single stranded Fv region. The reshaped Fv region has low human antigenicity, and is therefore expected to be useful as an agent for the diagnosis and treatment of cerebral tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                    Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21-g(gamma)1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reshaped anti-human myeloblastoma cell human antibody - has low human antigenicity, and is therefore useful for diagnosis and treatment of cerebral tumours, e.g. myeloblastoma
                                                                              Murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fv region; low human antigenicity; diagnosis; treatment; cerebral tumour; reshaped.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.8%; Score 523; DB 17;
83.7%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Pages 38-39; 45pp; Japanese.
                                                                                                                                                                          1..19
/label = sig_peptide
                                                                                                                                                                                                     20..136
/label= mat_peptide
                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                       69..85
/label- CDR_2
                                                                                                                                                                                                                               50..54
/label- CDR_1
                                                                                                                                                                                                                                                                                 118..125
/label= CDR_3
                                                                                                                                                                                                                                                                                                                                                                             94JP-0285057.
                                                                                                                                                                                                                                                                                                                                                                                                     94JP-0252166.
93JP-0291078.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHUS ) CHUGAI PHARM CO LID.
                             09-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-358509/36.
N-PSDB; AAT38653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g. myeloblastoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 136 AA;
                                                                                                                                                                                                                                                                                                                        JP08169900-A.
                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                           18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                   19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                   02-JUL-1996
                                                                                                                                    Synthetic.
  AAW04396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                          Peptide
                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                Key
    δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPKFQGRVTITADISASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 QYQLYQSGAEVKKPGSSVKVSCKASGENIKDTYIHWYRQAPGQGLEWMGRIDPADGNIKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ94539 encodes AAR76681 the human/murine chimeric antibody HEF-YL-M219(gamma). The antibody is reactive with human medulloblastoma (a brain tumour) cells. The chimeric antibody can be used in the diagnosis and treatment of this disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reconstituted antibody against human medullo:blastoma cells -contains high proportion of human antibody origin and has low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.8%; Score 523; DB 16; Length 136; Illarity 83.7%; Pred. No. 1.1e-40; Conservative 4; Mismatches 10; Indels
            Human; murine; chimeric antibody; HEF-RVL-M21g(gamma)1;
medulloblastoma; brain tumour; treatment; diagnosis.
                                                                             Jocation/Qualifiers
                                                                                                      /label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW04396 standard; Protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 26; Page 94; 120pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohtomo T, Sato K, Tsuchiya M;
                                                                                                                                                            'label= CDR 1
                                                                                                                                                                                                  70..86
/label= CDR 2
                                                                                                                                                                                                                                                                  CDR 3
                                                                                                                                                                                                                       87..118
/label= FR 3
                                                                                                                                                                      56..59
/label= FR 2
                                                                                                                      20..50
/label= FR 1
                                                                                                                                                                                                                                                                              127..136
/label= FR 4
                                                                                                                                                                                                                                                                                                                                                                           94WO-JP01763.
                                                                                                                                                                                                                                                                                                                                                                                                   93JP-0291078
                                                                                                                                                                                                                                                                                                                                                                                                                            (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                    119..126
                                                                                                                                                                                                                                                                 /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-200347/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ94539
                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                      19-0CT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                   19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigenicity
                                                                                                                                                                                                                                                                                                                     WO9514041-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 VSS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSS 123
                                                                                                                                                                                                                                                                                                                                              26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                        Peptide
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Gaps

9

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Query Match
Best Local Similarity
        VSS 123
                       137 VSS 139
                                                                                                                                                                Synthetic
                                                                               AAW04397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                         eptide
                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                        Peptide
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       121
                                                RESULT 14
                                                       AAW04397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                       Plasmid pSCFVT7-hM21; human; ONS-M21 antibody; chimeric protein; medulloblastoma; brain tumour; treatment; diagnosis; Fv fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ94548 is the plasmid pSCFVT7-hM21, which encodes AAR76682 the human antibody ONS-M21 Fv fragment. The plasmid was used in the construction of an expression vector, contg. cDNA encoding a human/murine chimeric antibody, reactive with human medulloblastoma (a brain tumour) cells. The chimeric antibody can be used in the diagnosis and treatment of this disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                        cells -
has low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Reconstituted antibody against human medullo:blastoma contains high proportion of human antibody origin and antigenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.8%; Score 523; DB 16;
83.7%; Pred. No. 2.2e-40;
ive 4; Mismatches 10;
                                                                                                                                                                                               "heavy variable region"
                                                                                                                                                                                                                                "light variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 35; Pages 98-99; 120pp; Japanese.
                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                               /label= sig_peptide
                                                       AAR76682 standard; Protein; 269 AA.
                                                                                                        Human ONS-M21 antibody Fv fragment.
                                                                                                                                                                                                                "linker"
                                                                                                                                                                                                                                                                                                                                                 Ohtomo T, Sato K, Tsuchiya M;
                                                                                                                                                                                                                       155..269
/note= "light
262..269
/note= "FLAG"
                                                                                                                                                                                                                                                                                                 94WO-JP01763.
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                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 79.8'
Best Local Similarity 83.7'
Matches 103; Conservative
                                                                                                                                                                                                        140..154
                                                                                                                                                                                        23..139
                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-200347/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 AA;
                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ94548.
                                                                                       18-JAN-1996
                                                                                                                                                 domo sapiens
                                                                                                                                                                                                                                                                                                19-OCT-1994;
121 VSS 123
               134 VSS 136
                                                                                                                                                                                                                                                                 W09514041-A1
                                                                                                                                                                                                                                                                                                                .9-NOV-1993;
                                                                                                                                                                                                                                                                                 6-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                       AAR76682;
                                                                                                                                                                       Peptide
                                                                                                                                                                                                                        Region
                                                                                                                                                                                        Region
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                                       RESULT 13
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The present sequence is a scFv fragment from the chimaeric human/murine monoclonal antibody (MAb) ONS-M21. The MAb was preped by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAb, with human light and heavy constant region sequences, respectively to produce chimaeric human/murine light and heavy chain DNA mols. A recombinant vector of for the expression of the heavy and light chain DNA mols. was prepd., and used to transform a host cell. The host cell was then cultured, and the expression prods. of the heavy and light chain DNA mols. sepd. and connected with a peptide linker to produce a single stranded Fv region. The reshaped Fv region has low human antigenicity, and is therefore expected to be useful as an agent of the diagnosis and treatment of cerebral tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reshaped anti-human myeloblastoma cell human antibody - has low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human antigenicity, and is therefore useful for diagnosis and
treatment of cerebral tumours, e.g. myeloblastoma
                                                                                                                                                                                                                                                                    Murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fv region; low human antigenicity; diagnosis; treatment; cerebral tumour; reshaped.
                                                                                                                                                                                                             Chimaeric human/murine MAb ONS-M21 scFv fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "heavy variable region"
140..154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "light variable region"
262..269
/label= FLAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= sig_peptide
AAW04397 standard; Protein; 269 AA.
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155..261
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                                                                                                                                     09-DEC-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT38662.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-OCT-1994;
19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-NOV-1994;
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Length 269;

Score 523; DB 17; Pred. No. 2.2e-40;

79.8%; 83.7%; ä

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                                                                                                                         DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
     Gaps
                                                       23 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 82
                                   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for treating inflammatory diseases such as multiple sclerosis. I can also be used in the treatment of stroke, cerebral traumas, maningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                            Humanized VLA-4 antibody 21.6 heavy chain variable region, Hc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.
 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saldanha J;
 4; Mismatches
                                                                                                                                                                                                                                                                                                    AAR81325 standard; Protein; 119 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leger OJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95WO-US01219
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 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody engineering.
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                                                                                                                                                                                                   137 VSS 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-1994;
                                                                                                                                                                             121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9519790-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUL-1995.
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                                                                                                                                                                                                                                                                                                                                       AAR81325;
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Matches
                                                                                                        61
                                                                                                                                                                                                                                                                    RESULT 15
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Score 515; DB 16; Length 119; Pred. No. 5e-40;

78.6%; 82.9%;

Query Match Best Local Similarity

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        Matches
        102;
        Conservative
        5;
        Mismatches
        12;
        Indels
        4;
        Gaps

        QY
        1
        QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY
        60

        Db
        1
        QVQLVQSGAEVKKPGASVKVSCKASGENIKSYAMHWVRQAPGQRLEWMGWINAGNTRY
        60

        QY
        61
        DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYGNYGWYAMDYWGQGTLVT
        120

        QY
        61
        SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYFGS----GSNYWGQGTLVT
        116

        QY
        121
        VSS
        123

        QY
        121
        VSS
        119

        Db
        117
        VSS
        119
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Search completed: January 6, 2003, 13:15:18 Job time: 29.5758 secs

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January 6, 2003, 13:13:21; Search time 10.1879 Seconds (without alignments) 355.228 Million cell updates/sec
                                                                                                                                                                                        US-09-155-739-11
655
1 QVQLVQSGAEVKKPGASVKV......NYGVYAMDYWGQGTLVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                      262574
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                262574 seqs, 29422922 residues
                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                          Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                     Scoring table:
                                                                        OM protein
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                                                                                                               Run on:
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Issued_Patents_AA:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 11, Appl	٠.	17,	17,	, 6	6	4	4,	19,	132,	7 '66	Sequence 109, App	13,	13,	12,	12,	44,	44,	10,	10,	17,	14,	17,	41,	8, A	36,	59,
ID	US-08-561-521-11	PCT-US95-01219-11	US-08-561-521-17	PCT-US95-01219-17	US-08-561-521-9	PCT-US95-01219-9	US-08-561-521-4	PCT-US95-01219-4	US-08-871-488A-19	US-08-646-265A-132	US-08-646-265A-99	US-08-646-265A-109	US-08-561-521-13	PCT-US95-01219-13	US-08-561-521-12	PCT-US95-01219-12	US-08-561-521-44	PCT-US95-01219-44	US-08-561-521-10	PCT-US95-01219-10	US-08-290-592E-17	PCT-US95-10053-14	PCT-US96-09448-17	US-09-438-954-41	US-08-232-081B-8	US-09-025-769B-36	US-09-025-769B-59
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Length	123	123	142	142	123	123	140	140	120	117	136	269	119	119	119	119	125	125	119	119	117	117	117	119	118	120	120
% Query Match	100.0	100.0	100.0	100.0	84.3	84.3		83.1	79.9	79.8	79.8	•	٠	78.6	78.2	78.2	77.1	77.1	75.6	75.6	75.1	75.1	75.1	75.1	75.0	74.7	74.7
Score	655	655	655	655	552	552	544	4	523.5	523	523	523	515	515	512	512	505	202	495	495	492	492	492	492			489.5
Result No.	-	7	m	4	S	φ	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

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Gaps ö

Length 123; Indels

Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 123; Conservative 0; Mismatches 0;

Sequence 63, Appl Sequence 112, Appl Sequence 19, Appl Sequence 19, Appl Sequence 18, Appl Sequence 23, Appl Sequence 23, Appl Sequence 41, Appl Sequence 41, Appl Sequence 51, Appl Sequence 53, Appl			ıst Leukocyte	and Crew Suite 2000	. 25		
US-08-836-561-63 US-08-436-7117D-112 US-08-438-7117-112 US-08-633-877C-19 US-08-603-024-18 US-08-603-024-18 US-08-202-047-23 US-08-202-047-23 US-09-301-593-41 US-09-301-593-41 US-09-301-593-41 US-08-4836-561-74 US-08-4836-551-74 US-08-487-1330-53 US-08-487-1330-53 US-08-487-1330-53 US-08-483-333-63	ALIGNMENTS	8561521 		Townsend Khourie , Steuart Tower,	disk patible -DoS/MS-DOS elease #1.0, Version #1 A: US/08/561,521	: 424 N DATA: MBER: US/08/186,269A 25-UNN-1994 NFORMATION: William L. UMBER: 30,223	15270-14 ION: 11:
74.0 74.0		pplication 0299 MATION: Bendig, M Leger, Ol Saldanha,	APPLICANT: Jones, S. Tarran TITLE OF INVENTION: Humanized TITLE OF INVENTION: Adhesion P NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS:	iee: Townsend and One Market Plaz San Francisco California : USA	BLE FORM: Floppy BM PC COM STEM: PC atentin R ATION DAT	FILING DAIE: CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/O FILING DAIE: 25-UAN-1994 ATTONEY AGENT INFORMATION: NAME: Smith, William L. REGISTRATION NUMBER: 30,	CKET NUMBER: 100 INFORMAT 115-543-5603 5-543-5043 SEO ID NO: CTERISTICS: amino acids cid single single inear protein
29 484 86 31 484.5 32 484.5 32 484.5 32 484.5 33 484.5 33 484.5 33 484.5 33 484.5 34 481 481 481 481 481 481 481 481 481 48	RESULT 1	US-08-561-521-11, Sequence 11, A patent No. 584 GENERAL INFOR APPLICANT: APPLICANT: APPLICANT: APPLICANT:		ADDRESSEE: STREET: One CITY: San F STATE: Cali COUNTRY: US ZTP: 2110:		FILLING CLASSIF PRIOR APP APPLICA PRIOR APP ATTORNEY NAME: REGISTR	REFERENCE/DO TELECOMMUICAT TELEFAX: 41: TELEFAX: 41: INFORMATION FOR: SEQUENCE CHARA TYPE: amino STRANDEDNESS TYPE: amino STRANDEDNESS MOLECULE TYPE: US-08-561-521:11

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                                                                                                                                                                                                 61 DPKFQGRVTITADTSASTAYWELSSLRSEDTAVYYCAREGYYGNYGNYAMDYWGQGLLVT 120
0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
PCT-US95-01219-11
Sequence 11, Application PC/TUS9501219
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 2000
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OFTANTING SISIEM: PATENTING SISIEM: CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US -JAN-1994
ATTONNEY/AGENT INFORMATION:
NAME: SMITH, William L.
NAME: SMITH, William L.
NAME: 20-JAN-1994
ATTONNEY/AGENT INFORMATION:
NAME:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
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Best Local Similarity 100.0
Matches 123; Conservative
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MOLECULE TYPE: protein
PCT-US95-01219-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                            GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STAFE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 655; DB 2; Length 142; 100.0%; Pred. No. 1.6e-58; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 424
CLASSIFICATION: A24
PRIOR APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTONNEY AGENT INFORMATION:
NAME: Smith, William I.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15270-14
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PCT-US95-01219-17
Sequence 17, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
               ; Sequence 17, Application US/08561521
; Patent No. 5840299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Smith, William L. REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 415-543-9600
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Best Local Similarity
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US-08-561-521-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08561521
Patent No. 5840299
Patent No. 5840299
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
              APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECHONE: 415-543-9600
TELEFAX: 415-543-9603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 142 amino acids
TYPE: amino acid
APPLICANT: Saldanha, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0
Best Local Similarity 100.0
Matches 123; Conservative
                                                                                                                                         STREET: One main.
CITY: San Francisco
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MOLECULE TYPE: protein
PCT-US95-01219-17
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                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2: CLASSIFICATION:
                                                                                                                                                                                                                                         94105
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61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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GENERAL INFORMATION:
FOR THE BORDING MATY M.
FAPLICANT: Bendig, Mary M.
FAPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TILLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                            COMPUTER FALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NOTA:
APPLICATION NOTE: US/08/561,521
FILING DATE: US/08/561,521
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, William 10,223
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
ADPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match

84.3%; Score 552; DB 2;
Best Local Similarity 82.9%; Pred. No. 2.8e-48;
Matches 102; Conservative 11; Mismatches 10
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94105
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PCT-US95-01219-9
COUNTRY:
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94105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08561521
Patent No. 58401299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                84.3%; Score 552; DB 5; Length 123;
82.9%; Pred. No. 2.8e-48;
Live 11; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 15270-14
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                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Smith, William L. REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-9
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                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 82.9%
Matches 102; Conservative
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California
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CLASSIFICATION:
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61 DPKFQGRVTITADISASTAYMELSSLRSEDIAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
ITILE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                Length 140;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           Ouery Match
83.1%; Score 544; DB 2;
Best Local Similarity 82.6%; Pred. No. 2.1e-47;
Matches 100; Conservative 11; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application PC/TUS9501219 GENERAL INFORMATION:
  TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                               SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 415-543-9600
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amino acid
415-543-5043
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                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-4
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                                                                                                                                                                                                                           Query Match
Best Local Similarity
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83.1%; Score 544; DB 5; Length 140;

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61 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYNN-----QDYWGQGTTVT 114
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1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Indels
                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: OHTOMO, TOSHIHIKO
APPLICANT: SATO, KOH
APPLICANT: TSUCHIYA, MASAYUKİ
TITLE OF INVENTION: RESHARED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 523; DB 4;
Pred. No. 2.1e-45;
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                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53466/184
                                                                                                                                                                                     Sequence 132, Application US/08646265A Patent No. 6214973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LEMSTH: 117 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEGNER, Harold C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 79.8%;
Best Local Similarity 83.7%;
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                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS: ADDRESSEE: Foley & La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-646-265A-132
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                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                      D.C.
USA
                                                                                                                                                RESULT 10
US-08-646-265A-132
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                                                      121 VSS 123
                                                                                         118 VSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE TITLE OF INVENTION: ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THEIR USE IN ITLE OF INVENTION: PRETARGETING METHODS
                                                                                                                                                    61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 523.5; DB 4; Length 120;
Pred. No. 2e-45;
8; Mismatches 10; Indels 3
               10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: SEED and BERRY 6300 Columbia Center, 701 Fifth Avenue
; Pred. No. 2.1e-47;
11; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Sharkey Ph.D., Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 690022.527C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/871,488A FILING DATE: 09-JUN-1997 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/08871488A Patent No. 6358710 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             Reno, John M.
Mallett, Robert W.
Hylarides, Mark D.
Searle, Stephen M.J.
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82.9%;
                                                                                                                                                                                                                                                                                                                                                                                               Graves, Scott S.
82.6%;
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Pedersen, Jan T.
Rees, Anthony R.
                 Matches 100; Conservative
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Matches 102; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and I
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STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-08-871-488A-19
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 Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Gaps

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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION:
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INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
                                                                                                                                                                                     COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-646-265A-109
                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                         APPLICANT: OHTOMO, TOSHINIKO
APPLICANT: SATO, KOh
APPLICANT: SATO, KOh
APPLICANT: SATO, KOh
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION UNBER:
PRILING DATE: 19-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19-0CT-1934
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELERX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 109, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, TOShihiko
               US-08-646-265A-99; Sequence 99, Application US/08646265A; Patent No. 6214973; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 83.7
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                      CITY: Washington
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RESULT 11
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Query Match 79.8%; Score 523; DB 4; Length 269;
Best Local Similarity 83.7%; Pred. No. 5.7e-45;
Matches 103; Conservative 4; Mismatches 10; Indels 6; Gaps
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Patent No. 5840299
EADERL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Loger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: 446bssion Molecule VLA-4
NUMBER OF SEQUENCES: 45
APPLICANT: SATO, KOh
APPLICANT: TSUCHIYA, MASAYUKI
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: WO PCT/JP94/01763
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 19-OCT-1994
PRIOR APPLICATION NUMBER: US 5-291078
FILING DATE: 19-NOV-1993
ATPORNEY/AGENT INFORMATION:
NAME: WEGENER, HACOTA 103.
RECISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
                                                                                                                 STREET: 8000 K Street, N.W., Suite 500 CIT: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.6%; Score 515; DB 2; Length 119; 82.9%; Pred. No. 1.4e-44;
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITH: San Francisco STATE: Callfornia
                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELEPHONE: 415-543-5600
TELEFRONE: 415-543-5600
                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,52
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                    STATE: CA
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61 DPKFQGRVTITADISASTAYMELSSLRSEDIAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQRLEWMGWINAGNITKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 OVOLVOSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGORLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldannia, Jose
APPLICANT: Soldannia, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 78.6%; Score 515; DB 5; Length 119; Best Local Similarity 82.9%; Pred. No. 1.4e-44; Matches 102; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STAATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                          омыЕК: PCT/US95/01219
25-JAN-1995
                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTONEX/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08561521 Patent No. 5840299 GENERAL INFORMATION:
                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                            CLASSIFICATION:
                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 78.2%; Score 512; DB 2; Length 119; Best Local Similarity 82.9%; Pred. No. 2.7e-44; Matches 102; Conservative 4; Mismatches 13; Indels
NAME: Smith, William L.

REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEPHONE: 415-543-9600
TELEPHONE: 415-543-9600
TELEPHONE: 415-543-9600
TELEPHONE: 415-543-9600
TELEPHONE: 415-543-5613
FENGRATION FOR SEO ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: January 6, 2003, 13:19:10
Job time: 11.1879 secs
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NAME: Olstein, Elliot M. REGISTRATION NUMBER: 24,025
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 117 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 86, Appl
Sequence 77, Appl
Sequence 18, Appl
Sequence 1, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 17, Appli
Sequence 13, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
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Sequence 1, Appli
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Sequence 2, Appli
                                                                                January 6, 2003, 13:17:36; Search time 5.96364 Seconds (without alignments) 390.875 Million cell updates/sec
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Sequence 53,
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                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKV......NYGVYAMDYWGQGTLVTVSS 123
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOG_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOG_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_USW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USOB_USW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_USW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USOB_USW_PUB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                               117078 seqs, 18951520 residues
                                                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                           length: 0
length: 2000000000
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Match Length
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                                                                                                                                                                                                    Scoring table:
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469
469
459.5
457
457
451.5
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448.5
447.5
447.5
446.5
446.5
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Maximum DB
                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                 Searched:
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                                                                                   Run on:
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Sequence 2, Applisequence 9, Applisequence 17, Applisequence 18, Applisequence 63, Applisequence 63, Applisequence 64, Applisequence 64, Applisequence 66, Applisequence 66, Applisequence 81, Applisequence 81, Applisequence 81, Applisequence 81, Applisequence 81, Applisequence 63, Applisequence 64, A
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
TITLE OF INVENTION: Respiratory Syncytical Virus
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
CITY: NEW JERSEY
              US-10-047-542-47

US-09-976-118-2

US-09-911-737-17

US-09-911-737-17

US-09-911-737-17

US-09-956-206A-78

US-09-956-206A-78

US-09-956-206A-18

US-09-956-206A-18

US-09-956-206A-18

US-09-825-012-66

US-09-825-012-76

US-09-825-012-76

US-09-825-012-90

US-09-825-012-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: P160
OPERATING SYSTEM: Windows95
SOFTWARE: MS WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,120A
FILLING DATE: September 21, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,592
FILING DATE: August 15, 1994
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/09158120A
Patent No. US20020102257A1
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 07000
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
^AMDITTER: P160
                                       USA
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973-994-1744

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FEATURE:
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                                                                                                                                                                                                                             61 DPKFQGRVTITADISASTAYMELSSLRSEDIAVYYCAREGYYGNYGVYAMDYWGQGTLVI 120
                                                                                                                                                                                                                                                  61 DPRFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYCA-----YYGTSSFDFWGQGTTLT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AQKFQGRVTMTRDKSSSTAYMELSSLRSEDTAVYYCAR---WGGDGFYAMDYWGQGTLVT 117
                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYXIXWVRQAPGQGLEWIGWIDPENGNIVF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
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                                                                                                                                                    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                         Query Match 75.1%; Score 492; DB 10; Length 117; Best Local Similarity 78.0%; Pred. No. 2.5e-33; Matches 96; Conservative 7; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Brettman, Lee R.
APPLICANT: Fox, Judith A.
APPLICANT: Allison, David Edward
APPLICANT: Allison, David Edward
TITLE OF INVENTION: Method of Administering an Antibody
PILE REFERENCE: 1855.2007-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/748,960 CURRENT FILING DATE: 2000-12-27 PRIOR APPLICATION NUMBER: US 09/550,082 PRIOR FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10025687 Patent No. US20020142255Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09748960
Patent No. US20010046496A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
            , MOLECULE TYPE: PROTEIN US-09-158-120A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 14
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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US-10-025-687-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-748-960-6
                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 QVQLVQSGAEVKKPGASVKVSCKGSCYTFTSYWMHWVRQAPGQRLEWIGEIDPSESNTNY 79
                                                                                                                                                       OTHER INFORMATION: Portion of the heavy chain of LDP-02 with a heavy OTHER INFORMATION: chain signal peptide
                                                                                                                                                                                                                                                                                                                                           Length 180;
                                                                                                                                                                                                                                                                                                                                     Ouery Match 73.9%; Score 484; DB 10; Length 18 Best Local Similarity 76.4%; Pred. No. 1.6e-32; Matches 94; Conservative 9; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-753-436-53
Sequence 53, Application US/09753436
Sequence 53, Application US/09753436
Sequence 53, Application US/09753436
SEMERAL INSORATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                         NAME/KEY: SITE

LOCATION: (19)...(20)

OTHER INFORMATION: signal peptide cleavage site
US-09-748-960-6
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-ANG-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
APPLICATION NUMBER: US 08/487,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-UN-1992
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/382,289
                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
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                                                    LENGTH: 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                  72.2%; Score 473; DB 10; Length 123; 78.0%; Pred. No. 8.7e-32; Live 7; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 86, Application US/09753436
Patent No. USZ0010029293A1
GENERAL INFORMATION:
GADIACANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION
                                                         APPLICATION NUMBER: US 07/827,689 FILING DATE: 27-JAN-1992 ATTORNEY/AGENT INFORMATION: NAME: Williams, Joseph A., Jr. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of America ZIP: 60606-6402
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JMBER: US 07/889,724
26-MAY-1992
                                                                                                                                                     REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/382,289
                                                                                                                                                                                                           TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
TYPE
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Best Local Similarity 78.03
Matches 96; Conservative
                        FILING DATE: 26-MAY-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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APPLICATION NUMBER:
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    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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CITY: Chicago
STATE: Illinois
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CLASSIFICATION:
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TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE MCTANININI RECOMBINANT PEPTIDES DERIVED FROM THE MCA ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND METHODS OF HUMANIZING ANTIBODY PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.1%; Score 472; DB 10; Length 123; Best Local Similarity 77.2%; Pred. No. 1e-31; Matches 95; Conservative 8; Mismatches 16; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTY: USA
ZIE: 94304-1018
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/956,206A
FILING DATE: 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page M111 Road
                                                                                                          PELICATION NUMBER: US 07/894,061
FILING DATE: 05-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-DAN-1992
ATTORNEY AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DO COUTO, FERNANDO J.R.
                                           us 08/009,266
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Sequence 77, Application US/09956206A;
Patent No. US20020164339A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        NAME: Williams, Joseph A., Jr. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            : LELEFAX: (312) 474-6300
: TELEFAX: (312) 474-6448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 86: SEQUENCE CHARACTERISTICS:
LENGTH: 123 amin -- TYPE
FILING DATE: 05-AUG-1993
                                                                 22-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
STATE: CA
                                                                 FILING DATE: 22-JAN-1 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-09-753-436-86
                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Sequence 28, Application US/09859053
Patent No. US20020102658A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Tecuka, Katsunari
APPLICANT: Hori, No. US20020102658A1uaki
APPLICANT: HORI, No. US2002010268A1uaki
APPLICANT: HORITON: HURAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: PARMAGEUTICAL USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YAQKFQGRVTITADISTSTAYAMELSSLRSEDTAVXYCARAPGYGGGGCYRGDYXFDYWG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 YDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGN----YGVYAMDYWG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDP-ANGYTK 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.6%; Score 469; DB 9; Length 129; 76.0%; Pred. No. 1.9e-31; Live 3; Mismatches 22; Indels
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                                                                                                                                                                                                                                                                                 NAME: WITT, ERIC
REGISTRATION NUMBER: 44,408
REFERENCE/DOCKET NUMBER: 276332000101
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 813-560
TELEFAX: (650) 494-0792
TELEFAX: 70611
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
             PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/525,539
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/US95/11683
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: 08/487,598
FILING DATE: 7-UNE-1995
APPLICATION NUMBER: 08/307,868
FILING DATE: 16-SEPT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 77: US-Q9-956-206A-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: UP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: UP 2000-147116
PRIOR FILING DATE: 2000-05-18
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
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ORGANISM: Homo sapiens
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Best Local S
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Matches

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TITLE OF INVENTION STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/025,687
CURRENT FILING DATE: 2002-04-17
WUMBER OF SEC ID NOS: 28
SOFTWARE: PARENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR PREVENTION OF ACUTE ORGAN DAMAGE AFTER EXTRACORPOREAL BLOOD CIRCULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Human consensus antibody heavy chain variable region us\hbox{-}10\hbox{-}025\hbox{-}687\hbox{-}1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
                                                                                                                     80 AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARTYYYDSSGYYHDAFDIWGQGTM 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVY--AMDYWGQGTL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                        20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWYRQAPGQGLEMMGWINPHSGGTNY 79
1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 70.2%; Score 459.5; DB 12; Length 120; Best Local Similarity 77.2%; Pred. No. 1e-30; Matches 95; Conservative 2; Mismatches 23; Indels 3;
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MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09917410
Patent No. US20020098183A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10025687 Patent No. US2002014225541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York COUNTRY: U.S.A. ZIP: 10022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                      119 VTVSS 123
                                                                                                                                                                                                                                     140 VTVSS 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
LENGTH: 120
                                                                                                                                                                                                                                                                                                                               US-10-025-687-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence OTHER INFORMATION: of H chain V region version s of humanized OTHER INFORMATION: anti-HM1.24 antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCA----REGYYGNYGVIAMDYWGQG 116
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                                                                                                                                                                                                                                                                                                                                                                                                                      69.6%; Score 456; DB 1; Length 249; 70.9%; Pred. No. 4e-30; Live 11; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVESTIGATION INHIBITOR OF LYMPHOCYTE ACTIVATION
TITLE OF INVESTION INHIBITOR OF LYMPHOCYTE ACTIVATION
FILE REFERENCE: 053466/0295
CURRENT APPLICATION NUMBER: US/09/760,723
CURRENT FILING DATE: 2001-05-29
FRIOR FULING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
FRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PALENTIN Ver. 2.1
                                                                                                                                                 REFERENCE/DOCKET NUMBER: P0986P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09760723 Patent No. US20020034507Al GENERAL INFORMATION:
                                          08/585005
                                                                                                         NAME: Lee, Wendy M. REGISTRATION NUMBER: 40,378
                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                              TELEPHONE: 415/225-1994
TELEFAX: 415/952-981
TELEX: 910/371-7168
INFORMATION FOR SO 1D NO: 48:
SEQUENCE CHARACTERISTICS:
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ORGANISM: Artificial Sequence
                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/55
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               LENGTH: 249 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 70.9%
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 72.48
Matches 92; Conservative
FILING DATE: 06/20/96
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                                                                                                                                                                                                                                                                                                                                    TYPE: Amin
TOPOLOGY:
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US-09-760-723-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 69.8%; Score 457; DB 10; Length 448; Best Local Similarity 75.6%; Pred. No. 5.8e-30; Matches 93; Conservative 8; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kyung, Jin Kim
APPLICANT: Matthews, Milliam
APPLICANT: Matthews, Maria L.
TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
COMRESPONDENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  NAME: Hanson, No. US20020098183Alman D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: 3.5 inch, 1.44 Mb floppy disk IBM PC compatible
                                                                                                                                                    APPLICATION NUMBER: 08/578,953
FILLING DATE: CIRKnown>
FILLING DATE: TRICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/917,410
FILING DATE: 26-Jul-2001
CLASSIFICATION: <unknown>
                       SOFTWARE: ASCII, WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 448 amino acid residues TYPE: amino acid
  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-917-410-6
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CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Chiang, Nancy Y.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                   PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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SOFTWARE: WinPat
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US-08-779-457-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence of H chain V region version r of humanized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 QVQLVQSGAEVKKPGASVKVSCKASGYTFTPYWMQWVRQAPGQGLEWMGSIFPGDGDTRY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence H chain V region version s of OTHER INFORMATION: anti-HM1.24 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 139;
                                                                                                                                                                                                                              APPLICANT: KOISHIRARA, YASUO
APPLICANT: KOISHIRARA, YASUO
APPLICANT: YOSHIMURA, YASUO
APPLICANT: YOSHIMURA, YASUO
TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
FILE REFERENCE: 053466/0255
CURRENT APPLICATION NUMBER: US/09/355,925
CURRENT APPLICATION NUMBER: PCT/JP98/00568
PRIOR PPLICATION NUMBER: PCT/JP98/00568
PRIOR FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: JP 9-41410
PRIOR FILING DATE: 1997-02-12
NUMBER OF SEO ID NOS: 8
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Patent No. US20020034507A1
GENERAL INFORMATION:
APPLICANT: KOISHHARA, YASUO
TITLE OF INVENTION: INHIBITOR OF LYMPHOCYTE ACTIVATION
FILE REFERENCE: 053466/0295
CURRENT FALLING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oulery Match 68.9%; Score 451.5; DB 10
Best Local Similarity 72.4%; Pred. No. 5.2e-30;
Matches 92; Conservative 6; Mismatches 18
                                                                                                                                                               ; Sequence 8, Application US/09355925
; Patent No. US20020037288A1
; GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
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                                            133 TTVTVSS 139
117 TLVTVSS 123
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                                                                                                                RESULT 12
US-09-355-925-8
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LENGIH: 139
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61 DPKFQGRVIITADISASTAYMELSSLRSEDIAVYYCA----REGYYGNYGVYAMDYWGQG 116
                                                                                                                                                                                                                                                                                                                                                            80 SQKFKGRVIMIADKSTSTAYMELSSLRSEDTAVYYCARGLRRGGYY-----FDYWGQG 132
                                                                                                                                                                                                                                         10 QVQLVQSGAEVKKPGASVKVSCKASGYTFTPYWMQWVRQAPGQGLEWMGSIFPGDGDTRY 79
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                                                                                                                                                     18; Indels 11; Gaps
                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Amino acid; OTHER INFORMATION: sequence of H chain V region version r of; OTHER INFORMATION: humanized anti-HMI.24 antibody US-09-355-925-7
                                                                                       Score 448.5; DB 10; Length 139;
Pred. No. 9e-30;
7; Mismatches 18; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 68.5%; Score 448.5; DB 10; Length 139; Best Local Similarity 71.7%; Pred. No. 9e-30; Matches 91; Conservative 7; Mismatches 18; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KOISHIHARA, YASUO
APPLICANT: YOSHIMURA, YASUO
APPLICANT: YOSHIMURA, YASUSHI
TITLE OF INVENTION: THERAREDTIC AGENT FOR LYMPHATIC TUMORS
FILE REPRENCE: 053466/0255
CURRENT APPLICATION NUMBER: US/09/355,925
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: PCT/JP98/00568
PRIOR FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: JP 9-41410
PRIOR FILING DATE: 1997-02-12
; OTHER INFORMATION: anti-HM1.24 antibody US-09-760-723-7
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APPLICANT: Athwal, Dilect Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/09949559
Patent No. US20020151682A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 7, Application US/09355925
; Patent No. US20020037288A1
                                                                                          68.5%;
71.7%;
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Best Local Similarity 71.7%
Matches 91; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                117 TLVTVSS 123
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Search completed: January 6, 2003, 13:29:32 Job time : 6.96364 secs

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Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2003
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OM protein - protein search, using sw model

6, 2003, 13:12:26 ; Search time 11.4303 Seconds
 (without alignments)
 1034.490 Million cell updates/sec January Run on:

US-09-155-739-11 655 Title: Perfect score: Sequence:

1 QVQLVQSGAEVKKPGASVKV.....NYGVYAMDYWGQGTLVTVSS 123

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* PIR_73:* .. Database

pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ď			SUMMAKIES	
Result	1	Query			;	
Q	Score	Match	Length	g ;	ID	Description
-	488.5		178	7	S29594	Ig gamma chain (WM
7	477	72.8	120	~	S03471	מ
m	473.5		118	7	S36265	Ig heavy chain V r
4	468		123	~	D33548	ь
'n	467		142	~	A32483	Ig heavy chain V r
9	465	71.0		~	S17586	Ig heavy chain V r
7	ഗ	70.2		~	S06823	. 50
8	456.5	69.7		7	PH0954	Ig heavy chain V r
6	455	69.5		7	S24289	g gamma ch
	455	69.5		7	S49220	Ig gamma-1 chain -
11	450	68.7		7	546393	Ig heavy chain V r
12	449	68.5		7	S03482	6
13	447.5	68.3	135	7	849530	'n
14	447	68.2		7	S03484	Ig heavy chain V-D
15	446.5	68.2		7	РН0960	Ig heavy chain V r
16	4	67.8		7	S04576	Ig heavy chain pre
17	-	9.79		7	PH0961	heavy chain
18		67.4		7	A56446	Ig heavy chain v r
19	439.5	67.1		7	PH1665	heavy cha
20		67.1		4	A47271	nitrophenyl phosph
21	e	67.0		~	C33548	Ig heavy chain V-1
22	43	67.0		7	S14683	Ig mu chain precur
23		6.99		~	PH1667	heavy
24		6.99		~	PH1666	Ig heavy chain V r
25		9.99		~	S52445	heavy
26		9.99		7	S31999	heavy
27	35.	66.5	120	7	PH0962	heavy cha
28		66.5		~	PH0952	Ig heavy chain V r
29		66.2		7	B33548	Ig heavy chain V-1

RESULT 2
S03471
Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S03471; S07453
R;Rocca Serrar J: Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Pougereau, EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-hypervariable regions.
A;Reference number: S03471; MUID:84057768; PMID:6416834

> g δ qq δ g

||| VSS 131 121 VSS 123

129

A; Accession: \$03471
A; Molecule type: mRNA
A; Residues: 7-120 <ROC1>
A; Construction of the first of the fir

J. Immunol. 129, 2554-2558, 1982 A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not

Iq heavy chain V r	, q	heavy chain v	neavy	heavy chain V	heavy		heavy chain					Ig heavy chain V r			heavy	chain V	ALIGNMENTS				06-Jan-1995 #text_change 05-Nov-1999			repruary 1991					:590; PIDN:CAA40992.1; PID:g52591	488	ed. No. 1.2e-36; Mismatches 14; Indels 5; Gaps 2;
PH0955	50000	144151	144131	PHIUIZ	PH0957	ETHUND	868170	A33548	S34014	836260	PH1561	S23623	S38950	S40295	PH1426	S20783	ALIC		1	(house (Iragment)	Ē								NID:952590;	Score	Pred. 11; Mi
7	c	۰ ۱	۹ (7	~	-	~	7	~	7	7	~	~	N	7	7			4	I ĕ	re			Library,					57;	, e 9	••
127	125	126	9 0	801	125	143	125	129	127	129	147	171	246	446	122	121				(house	sequence_revision				2 20				L:X578! lin		larity 75.6% Conservative
66.1	, 99	00.T	2 1	97.0	65.5	65.3	65.2	65.2	65.0	64.9	64.8	64.8	64.3	64.3	64.2	64.1				(wmos) - mouse (Iragme musculus (house mouse)	#	9594	i	Submitted to the EMBL Data		minary	: mRNA	78 <sey></sey>	A;Cross-references: EMBL:X57857; C;Keywords: immunoglobulin		ī
433	433	453	1000	4.29.5	4.29	427.5	427	427	426	425	424.5	424.5	421	421	420.5	420		_	4	s: Mus	06-Jan-	ion: S2	ır, R.	ed to th	A: Accession: S29594	A; Status: preliminary	A; Molecule type: mRNA	A; Residues: 1-178	referen ds: imm	Query Match	cocal Sir ss 93;
30	23	T 6	3 0		34	35	36	37	38	39	40	41	42	43	44	45		RESULT 1		C; Species: Mus	C; Date: 06-Jan-1995	C; Access	R; Seymour, R.	Submitte	A: Access	A; Status	A; Molecu	A; Residu	A; Cross C; Keywor	Query	Best Lo Matches

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93; Conservative
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A;Status: preliminary
A;Molecule type: mRNA
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C; Species: Homo sapiens: (man).
C; Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C; Accession: D33548
R; Aidles: T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A; Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A; Reference number: A33548; MUID:89345575; PMID:2503826
A; Accession: D33548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CiSpecies: Homo sapiens (man)
CiDate: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
CiAccession: 536265
RiGiffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; PMID:7679990
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                                                                                                                                                                                                                                                                                                   A; Residues: 1-11 CRIP>
A; Cross-references: RABL:218846; NID:933121; PIDN:CAA79298.1; PID:933900
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology
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                                                                                                                                                                                 Length 120;
                A;Accession: S07453
A;Molccule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                               15; Indels
A; Reference number: S07453; MUID:83058021; PMID:6815271
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                                                                                                                                                                              Score 477; DB 2;
Pred. No. 8.8e-36;
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75.6%;
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C; Species: Homo sapiens (man)
C; Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
R; Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck
Blochem. Blophys. Res. Commun. 160, 1250-1256, 1989
A; Title: Rapid clouing of rearranged immunoglobulin genes from human hybridoma cells
A; Reference number: A32483; MUID:89273586; PMID:2499327
A; Reference number: A32483; MUID:89273586; PMID:2499327
A; Accession: A32483
A; Molecule type: mRNA
A; Residues: 1-142 < LAR>
A; Molecule type: mRNA
A; Residues: 1-142 < LAR>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 25-108/Domain: immunoglobulin homology < LNM>
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C;Species: Mus musculus (house mouse)
C;Species: 22.Nov-1993 #sequence_revision 26.May-1995 #text_change 21-Jan-2000
C;Accession: S17586
R;MyIvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A;Title: Blochemical implications from the variable gene sequences of an anti-cytochr
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                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                        Length 123;
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A;Molecule type: mRNA
A;Residues: 1-123 <KIFP
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                           Query Match 71.5%; Score 468; DB 2; Length 12
Best Local Similarity 74.8%; Pred. No. 5.7e-35;
Matches 92; Conservative 7; Mismatches 24; Indels
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A; Accession: S17586
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114 VSS 116
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S24289
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J. Mol. Biol. 209, 763-778, 1989
Affitle: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A. Reference number: S06815; MUID:90064531; PMID:2555519
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C.Bate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C.Bate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
R.Bartin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J.Exp. Med. 175, 983-991, 1992
A.F.Itle: Evidence for somatic selection of natural autoantibodies.
A.Reference number: PH0952; MUID:92202880; PMID:1552291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region (clone IIc) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                             61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY-YGNYGVYAMDYWGQGTLV 119
                                                                                                                                                                                                                                                                                                                   61 DPRFQDKATITADISSNTAYLQLSSLTSEDTAVYCA--GYDYGNF----DYWGQGTTL 113

    60 YDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLV 119

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               A;Cross-references: EMBL:X60683; NID:g51820; PIDN:CAA43095.1; PID:g51821
C;Superfanily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                         Length 117;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                   11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.2%; Score 459.5; DB 273.4%; Pred. No. 3.3e-34;
                                                                                                                         71.0%; Score 465; DB 2 72.6%; Pred. No. 1e-34;
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                                                                                                                                                                   15; Mismatches
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A;Molecule type: DNA
                                                                                                                                         Best Local Similarity 72.6%
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 73.49
Matches 91; Conservative
A; Residues: 1-117 <MYL>
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Gramma-1 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C;Accession: S49220
R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
Submitted to the EMBL Data Library, September 1994
A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing A;Reference number: S49220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, September 1991
A; Description: Cloning and sequencing of the cDNA coding for the variable regions of
A; Reference number: S24287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Cross-references: EMBL:X62705; NID:g51690; PIDN:CAA44584.1; PID:g1333963 C. Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYD 61
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                                                                                                                                                                                                                                                                   Length 132;
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                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                                                                                                   DB 2;
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Pred. No. 7.8e-34;
                                                                                                                                                                                                                                                             ch 69.7%; Score 456.5; DB 2
1 Similarity 72.0%; Pred. No. 6.6e-34;
95; Conservative 1; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches
                                                                                                                                           F;51-67/Region: complementarity-determining 2 F;68-98/Region: framework 3 F;99-120/Region: complementarity-determining 3
                                                                                      F;31-35/Region: complementarity-determining F;36-50/Region: framework 2
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IN
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Best Local Similarity 71.5%
Matches 88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 YWGQGTLVTVSS 123
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Best Local Similarity
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-116 < MON>
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A; Note: this sequence was determined from the differentiated gene R; Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug J. Immunol. 129, 2554-2558, 1982
A;Tille: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not A;Reference number: S07453; MUID:83058021; PMID:6815271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYC -- AREGYYGNYGVYAMDYWGQGTL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARARTGY------NYWGQGTL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEMMGWINPNSGCTNY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 115;
                                                                                                                                                                                                                                                                                           A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-43 <ROC2>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                  68.5%; Score 449; DB 2; Length 115
70.2%; Pred. No. 2.7e-33;
Live 12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
              A; Reference number: $03471; MUID: 84057768; PMID: 6416834 A; Accession: $03482
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72.8%; Pred. No. 4.3e-33;
iive 7; Mismatches 16
                                                                                        A;Molecule type: mRNA
A;Residues: 10-115 <ROC1>
A;Cross-references: EMBL;X03219
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 70.28
Matches 85; Conservative
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Best Local Similarity
  hypervariable regions
                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                               A; Accession: S07453
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A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAJ
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(S.Species: Mus musculus (house mouse)
A;Variety: strain BALB/C
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: 803482; 807453
R;Rocca-Serra, J; Antthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M. EMBO J. 2, 867-872, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ririgini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.

7. Mol. Blol. 239, 68-78, 1994

A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by A;Reference number: $46390; MUID:94254092; PMID:8196048
                                                                                                                                                                                                                                                                             1;
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C;Dàte: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Cross-references: EMBL:231680; NID:9509786; PIDN:CAA83485.1; PID:91335146 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F:15-98/Domain: immunoglobulin homology <IMM>
                                        A;Cross-references: EMBL:237502; NID:9541778; PIDN:CAA85732.1; PID:9541779 A;Experimental source: strain Balb/c C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AQKFQGWVTMTRDTSISTAYMELSRLRSDDTAVYYCARDSAYYYDSSGYXSANYYMDWG 120
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                                                                                                                                    F;1\frac{1}{120}/Domain: V region #status predicted <VRG>F;1\frac{2}{1}-221/Domain: C region #status predicted <CRG>F;1\frac{3}{9}-203/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-129 <FIG>
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A; Molecule type: mRNA
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Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment) C:Species: Was musculus (house mouse)	C. Date: 26-Feb-1998 #squence_revision 26-Feb-1998 #text_change 21-Jan-2000 C; Accession: S03484; S07453	R; Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M. EMBO J. 2, 867-872, 1983	A; Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT hypervariable regions	A; Reference number: S03471; MUID:84057768; PMID:6416834 A; Accession: S03484	A;Scatus: preliminary A;Wolecule type: mRNA A;Residues: 10-120 <roc1> A;Cross-references: EMBL:X07144 A;Note: this sequence was determined from the differentiated gene R;Rocca: Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere</roc1>	repertoire does	A; Wesidues: 1-43 <roc2> C; Superfamily: immunoglobulin V region; immunoglobulin homology F; 15-98/Domain: immunoglobulin homology <imm></imm></roc2>	Query Match 68.2%; Score 447; DB 2; Length 120; Best Local Similarity 71.5%; Pred. No. 4.2e-33; Matches 88; Conservative 11; Mismatches 20; Indels 4; Gaps 1;	OY 1 QVOLVOSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60 :	QY 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYCAREGYYCNYGVYAMDYMCQGTLVT 120 	0y 121 VSS 123 	RESULT 15 PH0960	Ig heavy chain V region (G6+ T-L30) - human (fragment) C;Species: Homo sapiens (man) C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996	K.Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J. J. Exp. Med. 175, 983-991, 1992 J. Mith. Pristons, S.	A, Tute: E. Futurice 101 Solmatic Selection of natural autoantibodies. A, Reference number: PH0952; MUID:92202880; PMID:1552291 A, Accession: PH0960	A.Status: nucleic acid sequence not shown A.Molecule type: DNA A.Residues: 1-136 <mar></mar>	C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F:1-30/Region: framework 1	F;15-98/Domain: immunoglobulin homology <imm> F;31-35/Region: complementarity-determining 1 F;36-50/Region: framework 2</imm>	F;51-67/Region: complementarity-determining 2 F:68-98/Region: framework 3 F;99-124/Region: complementarity-determining 3	Query Match 68.2%; Score 446.5; DB 2; Length 136; Best Local Similarity 69.1%; Pred. No. 5.3e-33; Matches 94; Conservative 1; Mismatches 28; Indels 13; Gaps 1;

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                                                                             108 YAMDYWGOGTLVTVSS 123
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 6, 2003, 12:48:25; Search time 6.21212 Seconds (without alignments) 821.231 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-155-739-11 655 1 QVQLVQSGAEVKKPGASVKV.....NYGVYAMDYWGQGTLVTVSS 123

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P01744 homo sapien	mus m	P01751 mus musculu	P01743 homo sapien	P01746 mus musculu	3 ното	12 homo	57 mus m	m	P01756 mus musculu	P01755 mus musculu	P03980 mus musculu	P06329 mus musculu	P01745 mus musculu	P01759 mus musculu	P06326 homo sapien	P80421 homo sapien	P01753 mus musculu	P01741 mus musculu	P01748 mus musculu	P01750 mus musculu	P01783 mus musculu	P01754 mus musculu	P01761 homo sapien	P01758 mus musculu	Bus	P06327 mus musculu	P01793 mus musculu	P01807 mus musculu	P01760 homo sapien	8 mus	8	P01768 homo sapien
SUMMARIES	ID	HV1C_HUMAN	HV03_MOUSE	HV07_MOUSE	HV1B_HUMAN	HV02_MOUSE	HV1G_HUMAN	HV1A_HUMAN	HV13_MOUSE	HV51_MOUSE	HV12_MOUSE	HV11_MOUSE	HV48_MOUSE	HV50_MOUSE	HV01_MOUSE	HV15_MOUSE	HV1F_HUMAN	HV1H_HUMAN	HV09_MOUSE	HV00_MOUSE	HV04_MOUSE	HV06_MOUSE	HV16_MOUSE	HV10_MOUSE	HV1E_HUMAN	HV14_MOUSE	HV49_MOUSE	HV52_MOUSE	HV24_MOUSE	HV37_MOUSE	HV1D_HUMAN	HV38_MOUSE	HV40_MOUSE	HV3G_HUMAN
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		.	puence update) iotation update) recursor (Fragments). Craniata; Vertebrata; Catarrhini; Hominidae;	Derbyshire he gene for h a myeloma 55(1982).	S.G.O., von Bahr-Lindstrom H.; ty: modern concepts and developr (1978). EPSILON CHAIN WAS ISOLATED FROM JAHC.	al. IG HEAVY CHAIN V-I REGION ND PYRROLIDONE CARBOXYLIC ACID. T -> V (IN REF. 2). IH -> HI (IN REF. 2). VG -> GV (IN REF. 2). MISSING (IN REF. 2). 948F9F72A5366C20 CRC64;	DB 1 25; 25 25 0APG QAPG
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Marshak-Rothstein A.;
The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";
Eur. J. Immunol. 12:1033-1034(1982).
-!- MISCELLANBOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                        Promiser Product; 19; 1. SMART; SMO0406; 1Gv; 1. Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 409; DB 1;
Pred. No. 1.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HV07_MOUSE STANDARD; PRT; 139 AA. P01751; P01752; 21-JUL-1986 (Rel. 01, Created) 15-JUL-1996 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Iq heavy chain V region B1-8/186-2 precursor.
                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Mismatches
                                                                                                                                                   Ig heavy chain V region 36-65.
                                                                                                                                                                                                                                                                                                                                          HSSP, P01789, 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                            62.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               77; Conservative
                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                       SEGMENT, JH2.
PIR; A02028; HVMSG7.
                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-C57BL/6;
                     116 GTLVTVSS 123
                                         140 GITVIVSS 147
                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS 123
                                                                                              HV03_MOUSE
P01747;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                   HV03_MOUSE
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                                                                            "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.", cell 24:625-637(1981).
-!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=81144028; PubMed=6298778;
Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V-I region HG3 precursor.

Mono saplens (Human).

Eukaryota; Metazoma; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION B1-8/186-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY - DETERMINING - 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15419 MW; 1B57DD4FD0C9F465 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.4%; Score 408.5; DB 1 62.6%; Pred. No. 2.4e-34;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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D SEGMENT.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J00529; AAA38170.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 62.68
Matches 77; Conservative
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                                                                                                                                                                                                                              (NPB ANTIBODIES).
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HSSP; P01810; 2FBJ.
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139 1
139 AA;
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                                                Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 VSS 123
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P01743;
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NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 117;
                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V-I REGION HG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                 117 117
117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;
                Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPKFQGRVTITADISASTAYMELSSLRSEDIAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Arel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                            Immunoglobulin V region; Signal.
                                                                                                                                                                                          EMBL; J00240; AAA52988.1; -.
                                                                                                                                                                                                                       HSSP, P01772, 2FB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 79.6
tes 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                          Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
(VH) gene subgroups.";
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                                                                                                                                                                                                        A02024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Capra J.D.;
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ID HV02_MOUSE
                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                          61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                 Gaps
                                                                                                                                                                 1 OVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-88296408; PubMed-2841108;
Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., 2ong S.Q.,
Ohno H., Fukuhara S., Honjo T.;
"Dispersed localization of D segments in the human immunoglobulin
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                      60.9%; Score 399; DB 1; Length 140; 61.0%; Pred. No. 2.2e-33; Ive 19; Mismatches 27; Indels
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                                             IG HEAVY CHAIN V REGION 93G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 117
117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;
                                                                         140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
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Pred. No. 3.7e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 20, Last sequence update)
(Rel. 38, Last annotation update)
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V-I region V35 precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last seq
15-JUL-1999 (Rel. 38, Last ann
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78.68;
                                                                                                                     61.0%;
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                                                                                                                                    75; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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140
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                                                                                                                       Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heavy-chain locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                       121 VSS 123
                                                                                                                                                                                                                                                                                                                    138 VSS 140
                                                                                                                                                                                                                                                                                                                                                                                            HV1G_HUMAN
P23083;
                                                           NON_TER
SEQUENCE
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                             SIGNAL
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                                               CHAIN
                                                                                                                                     Jatches
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Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.; "A V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes."; EMBO J. 3:517-523(1984).
PIR; A02040; MHMS38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DPKFQGRVT1TADTSASTAYMELSSLRSEDTAVYYCARECYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                           01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
11-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region AC38 205.12.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                      Query Match 57.7%; Score 378; DB 1; Length 117; Best Local Similarity 58.5%; Pred. No. 2.4e-31; Matches 72; Conservative 20; Mismatches 25; Indels
                                                                                                                                                                                   D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-84182519; PubMed-6201362;
                                                                MEDLINE=80078170; PubMed=6765983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01789; 1MCP
                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 VSS 117
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P06330;
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                                                    SEQUENCE
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                                                                                                                                                                                                                                                                   MEDLINE-71064024; PubMed-5489771; Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., Waxdal M.J., Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments HI-H4."; Biochemistry 9:3161-3170(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA----GGYGIYSPEEY-NGGLVT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DPKFQGRVTITADISASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRSAIIWVRQAPGQGLEWMGGIVPMFGPPNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                    The covalent structure of a human gamma G-immunoglobulin. X.

Intrachain disulfide bonds.";

Entrachain PRODES THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.

ENTRACHAIN PROTEIN HAS ALSO BEEN DETERMINED.

InterPro; IPRO30306; Ig_MRC.

InterPro; IPRO30306; Ig_W.

Entrachain PRO0047; ig, 1.

ENTROLIDONE CARBOXYLIC ACID.

ENTRACE SMON406; IGY: 1.

ENTROLIDONE CARBOXYLIC ACID.

ENTRACE TO SEQUENCE 117 AA; 12472 MW; 99D60ADAEBD52818 CRC64;
                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 heavy chain V-I region EU.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.5%; Score 390; DB 1; Length 117; 68.3%; Pred. No. 1.5e-32; artive 8; Mismatches 25; Indels
                        61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=71064027; PubMed=4923144;
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                                                                                                         STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                   DISULFIDE BOND.
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                                                                                                        HV1A_HUMAN
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P01757;
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                                    Gaps
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                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                      SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
MEDLINE-83075344; Pubmed-6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (COMPLEX).
                  DB 1; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.9%; Score 373; DB 1; Length 117
59.3%; Pred. No. 7.6e-31;
ive 19; Mismatches 25; Indels
                                    29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 55 N-LINKED (GLUGGER) 117 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;
118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
                57.3%; Score 375.5; DB 1; 58.5%; Pred. No. 4.3e-31; iive 17; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                    -i- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
PIR; A02039; MHMS4E.
HSSP; P01789; IMCP.
                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUN-2002 (Rel. 41, Last annotation update)
1g heavy chain V region MOPC 104E.
                                                                                                                                                                                        117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin V region; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                              PROTEIN HAS ALSO BEEN DETERMINED.
                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72; Conservative
                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                          Mus musculus (Mouse)
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                          121 VSS 123
                                                                                                                                           116 VSS 118
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P01756;
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SEQUENCE
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HV11_MOUSE
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                                    Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                    MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
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                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.7%; Score 371.5; DB 1
60.2%; Pred. No. 1.3e-30;
                                       (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
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137 AA
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JH2 SEGMENT.
                                       21-JUL-1986 (Rel. 01, Created)
1-JUL-1986 (Rel. 01, Last sequence upd
15-JUL-1999 (Rel. 38, Last annotation upd
19 heavy chain V region S43 precursor.
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  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; 19; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J00539; AAA38172.1; -. PIR; A02038; G2MS43. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_V.
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  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                         (NPB ANTIBODIES).
                                                                                                                              (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 AA;
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                         Baltimore D.;
                                                                                                                            Mus musculus
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HV11_MOUSE
P01755;
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ID HV48_MOUSE
AC P03980;
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SEQUENCE
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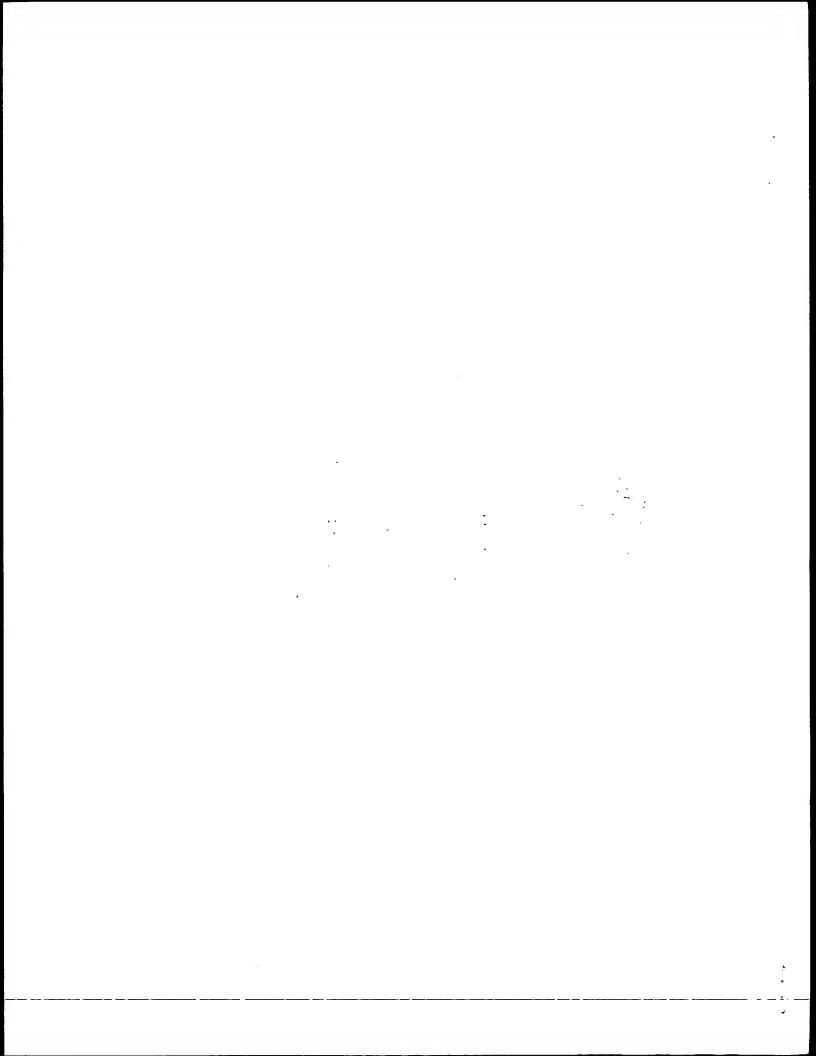
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                         MEDLINE-84248078; PubMed-6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.E.,
                                                                                                                 "Illegitimate recombination generates a class switch from C mu to C delta in an IgD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
PIR; A02033; HVMST7.
                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                HEAVY CHAIN V REGION TEPC 1017.
                                                                                                                                                                                                                                         FRAMEWORK - 1.
COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                                                                                                56.3%; Score 369; DB 1; Length 138; 58.1%; Pred. No. 2.3e-30; Live 20; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                        COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
                                                                                                                                                                                                                                                                       COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                15576 MW; 748157E4C6907B8E CRC64;
23-OCT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region AC38 15.3.
                   Ig heavy chain V region TEPC 1017 precursor.
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                                                                                                                                                                  InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
InterPro; IPR003596; Ig_V.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
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                                                                                                                                                                                                                                                                                                                                138 AA;
                                                                             SEQUENCE FROM N.A.
                                                                                                                                                            HSSP; P01810; 2FBJ
                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                           NCBI_TaxID=10090;
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P06329;
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Nucleic Acids Res. 8:4839-4840(1980).
-- MISCELLANBEUUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A MYELOMA THAT SECRETES IGG2B.
PIR; A02027; GVMS11.
                                                                                                                                                                                                                                                                                                                                                                                                                    61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                       DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-81053741; Pubmed-6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
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                                                                                                                                                                                                                                                      DB 1; Length 120;
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55.3%; Pred. No. 1.6e-29;
.ive 23; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                           13311 MW; 914453F426F09834 CRC64;
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                                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                    55.6%; Score 364.5; DB 1
56.1%; Pred. No. 5.6e-30;
iive 19; Mismatches 32
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region MPC 11.
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J SEGMENT.
BY SIMILARITY.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Matches 69; Conservative
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                                         Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region.
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105
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96
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106 1
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120 1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
SEQUENCE FROM N.A.
MEDLINE-82222222; Pubmed-6806821;
KRAPP M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                               "Simultaneous expression of immunoglobulin mu and delta heavy chains by a cloned B-cell lymphoma: a single copy of the VH gene is shared by two adjacent CH genes."

Proc. Natl. Acad. Sci. 0.S.A. 79:2996-3000(1982).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                        136 AA.
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Job time : 6.21212 secs
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL 1
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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P01759;
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SEQUENCE
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January 6, 2003, 13:10:51; Search time 23.1091 Seconds (without alignments) 1096.702 Million cell updates/sec
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655
1 QVQLVQSGAEVKKPGASVKV......NYGVYAMDYWGQGTLVTVSS 123
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	B ID Description	4 Q9UL92 homo sapien		1 099131 mus	11 Q9JL85 mus musculu			5 09GYZ2 schistosoma			Q9d814 mus			11 Q924R8 musculu	4 Q9UL89 homo sapien	11 092406 mis miscuil.
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ď	Query Match I	69.8	67.3	67.2	0.99	0.99	0.99	65.3	65.3	65.2	64.4	63.4	63.4	65.8	62.8	6.5
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17 408.5 62.4 473 11 099125 18 408 62.3 142 11 092401 19 407.5 62.2 143 11 092409 20 405.5 61.9 145 11 092409 21 405.5 61.9 145 11 0924R0 22 403.5 61.6 143 11 0924R0 24 403.5 61.6 143 11 0924R0 25 399 60.9 142 11 0924R0 26 399 60.9 142 11 0924R0 27 398 60.9 142 11 0924R0 28 398 60.8 481 11 0924R7 29 394.5 60.2 143 11 0924R7 39 389.5 59.8 488 11 0924R3 33 389.5 59.8 488 11 0924R3 34 388.5 59.5 137 11 0924R5 35 388.5 59.3 141 11 0924R4 37 388.5 59.3 141 11 0924C4 38 383.5 58.5 613 11 091C7 40 381.5 58.2 463 11 091C67 41 381.5 58.2 463 11 091C67 42 380 580 680 481 11 0924C6 43 380 580 680 481 11 0924C6 44 380 580 680 481 11 0924C6 45 380 580 680 481 11 091C67 46 381 580 680 481 11 091C67 47 381.5 58.2 463 11 091C67 48 380 580 680 481 11 0924C6	RESULT 1 09UL92 ID 01U-9AX-2000 (TrEMBLrel. 13, Last sequence update) DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) DT Myosin-reactive immunoglobulin heavy chain variable r DE (Fragment) OS Homo sapiens (Human) OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E OC Mammalia; Butheria; Primates; Catarrhin; Hominidae; OX NCBL_TAXID=9606; RN (1) RN EDLINE=98277139; PubMed=9614934; RA YOUNG D.C.; RY MYOSin-reactive autoantibodies in rheumatic carditis RT (Lin Immunol. Immunopathol. 87:184-192(1998). DR EMBL; AF03502; AAD56258.1; DR HSSP; P01772; 2FB4. DR InterPro; IPR003906; Ig_W. DR SEQUENCE 124 AA; 13580 WW; IBAAACBD96ACD2A2 CRC64 Ouery Match DES SAGRECE 124 AA; 13580 WW; Ox 2.88-40; Dest Local Similarity 69:8%; Score 457.5; DB 4; Len Best Local Similarity 69:8%; DR 00.28 Abthered Similarity 60:28 Abthered Similarity 60:28 Abt

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61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                 67.2%; Score 440; DB 11; Length 468; 67.5%; Pred. No. 1e-37;
                                                                                                                                                                       ; Pred. No. 1e-37;
16; Mismatches 20; Indels
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
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Infect. Immun. 68:5803-5808(2000).
EMBL; AF206021; AAF69319.1; -.
HSSP; P01810; 2FBJ.
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MEDLINE=20448942; PubMed=10992488;
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SWART; SMO0406; IGv; 1.
NON_TER 109 109
                                                                                                                                                                Best Local Similarity 67.59
Matches 83; Conservative
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hes 79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                   121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                             136 VSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UL94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9JL85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09UL94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9JL85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAM-----DY 112
                   61 AQKFQGRVTWITDISISINYELSSLRSEDTAVYYCAR-----GLYVVVPAAFSRFDY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 SQKFQGRLIMTRDISISTYYMDLSSLRSDDTAVYFCAREMEIIFGGAVSKGFY----YYG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DPKFQGRVTITADISASTAYMELSSLRSEDIAVYYCARE------GYYGNYGVYA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Mismatches 19; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVQLVQSGAEVKKPGASVKVSCKASGYIFSNYYMNWVRQAPGQGPEWMGVINPSGGSARY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tilson M.D.;
"Homo sapiens putative microfibrillar protein with Ig-like domain 3 mRNA (Matrix Call Adhesion Molecule-3, Mat-CAM 3).";
mRNA (Matrix 2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY039025; AAK82649.1;
Interpro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 1.
SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.3%; Score 440.5; DB 4; Length 159; 64.9%; Pred. No. 2.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BOORS, AAH03878.1;
HSRP; P01842; 7FAB.
InterPro; IPR003599; Ig.
InterPro; IPR003509; Ig.cl.
InterPro; IPR003500; Ig_like.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003506; Ig_WHC.
                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-UUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          468 AA.
                                                                                                                                                                                                                                                                                                                                     Putative matrix cell adhesion molecule-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 64.99
Matches 87; Conservative
                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 MDVWGQGTTVTVSS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 MDYWGQGTLVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; iq; 3.
                                                                                 WGQGTLVTVSS 123
                                                                                                                         114 WGOGTLVTVSS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                    096030;
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                                                                                 113
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Q96QS0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AQKFQGRVTMTKDTSISTAYMELSRLRSDDTAVYYCARGGGRGLW----FDPWGQGTLVT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                               Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MDELINE-99277139; Pubmed-9614934;
WU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.0%; Score 432; DB 4; Length 11 70.7%; Pred. No. 1.3e-37; Live 10; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submit BC009951; AAH09851.1;
InterPro: IPR000005; HTHARAC.
InterPro: IPR003598; Ig_c2.
InterPro: IPR003506; Ig_MHC.
Pfan; PF0047; 1g; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER 119 119
SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (Protein for MGC:15420).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035020; AAD56256.1; -.
HASP; P01810; 2FBJ.
INCEPPO; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         614 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.0%; Score 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin domain.
                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 VSS 119
                                                                                                                          (Fragment)
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                                                                                               Schistosoma japonicum (Blood fluke).
Bukaryota, Wetazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DPKFQGRVTITADISASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Song X.T., Feng Z.O., Guan X.H.;
Song X.T., Feng Z.O., Guan X.H.;
"Amplification, cloning and sequence analysis of the heavy chain variable region gene of monoclonal anti-idlotypic antibody NP30 of Schistosoma japonicum."
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF2826622; AAG01452.1;
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.3%; Score 428; DB 5; Length 119; 66.7%; Pred. No. 3.3e.37; ative 17; Mismatches 20; Indels
  71.5%; Pred. No. 9.9e-37;
ive 9; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 AA; 13567 MW; BA893873FD5FA6AB CRC64;
                                                                                                                                                                                                                                                             119 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003599; 19.
InterPro; IPR003600; 19_11ke.
InterPro; IPR003006; 19_MHC.
InterPro; IPR003596; 19_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEAM; PF00041; 19; 1.
PRINTS, PR01573; SUPERTUBBY.
SWART; SM00409; 16; 1.
SWART; SM00406; 16v; 1.
Best Local Similarity 71.5
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                         121 VSS 123
                                                                                                                                                                            138 VSS 140
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                                                                                                                                                                                                                                                                                                                                             Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duery Match
                                                                                                                                                                                                                                                                         09GYZ2;
                                                                                                                                                                                                                                                          Q9GYZ2
                                                                                                                                                                                                                             RESULT 7
Q9GYZ2
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Q9UL95
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Pfam; PF00047
                                                                                                                                     121 VSS 123
                                                                                                                                                                   119 VSS 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kozono Y., Kozono H., Azuma T.;

Kozono Y., Kozono H., Azuma T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3 Nitrophenyl) Acetyl (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB067797; BAB63282.1;

InterPro; IPR003006; Ig_MHC.

Pfam; PF00047; Ig; I.

NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            092403 PRELIMINARY; PRT; 146 AA.
092403;
09105C-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
WH186.2-D-J-C mu protein (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                      "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.2%; Score 427; DB 11; Length 146; ilarity 65.9%; Pred. No. 5.5e-37; Conservative 17; Mismatches 23; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                         65.3%; Score 428; DB 4; Length 125; 68.8%; Pred. No. 3.5e-37; Live 10; Mismatches 27; Indels
                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 AA; 16136 MW; CEA8DD6E1955807F CRC64;
                                                                                                                                                                                                                                                                                                                                                                           125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
                                                                                                                                                                                                                              EMBL, AF035019, AAD56255.1; -.
HSSP, PO1810; ZFBJ.
HSSP, PO1810; ZFBJ.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF0047; ig; 1.
SMART; SMO046; IG, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 68.89 nes 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
ses 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 VTVSS 123
                                                                                                                                                                                         Young D.C.;
                                                  (Fragment).
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SEQUENCE
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Matches
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092403
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REQUENCE FROM N.A.

SCENDING-27BL/6J; TISSUE-PANCREAS;

MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217851;

A Azawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Azawa T., Izawa M., Nishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa T., Izawa M., Nishi K., Isono H., Adachi J., Fukuda S.,

A Azawa T., Sator T., Sator T., Sator R.,

Radota K., Matsuda H.A., Ashburner M., Banalov S., Casawant T.,

Radota K., Matsuda H.A., Ashburner M., Boole G., Quackenbush J.,

Radota K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Satal K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Winshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nanabakishi,
                                                                                                                    61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                    4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003966; Ig_WHC.
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EMBL; AKO07918; BAB25349.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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IGH-1 OR 1810060009RIK.
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Gaps

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Matches

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Gaps

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DB 11; Length 145;

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61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                        63.4%; Score 415.5; DB 11; Length 64.2%; Pred. No. 8.7e-36; Live 16; Mismatches 25; Indels
            Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067789; BAB63274.1;
InterPro; IPR003006; Ig_MHC.
                                                                                                                 145 AA; 15979 MW; 0162D0A26C746C04 CRC64;
                                                                                                                                                                           79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                      145
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                                                                                                                                                              Similarity
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SEQUENCE
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(7)
                            20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kozono Y., Kozono H., Azuma T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Bydroxy-3-Nitrophenyl)Acetyl (NP).";

Submitted (AGG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL: AB067785; BAB63270.1;

Pfam; PF00047; 1g; 1.

NON-TER
                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.4%; Score 415.5; DB 11; Length 145; 65.0%; Pred. No. 8.7e-36; tive 17; Mismatches 23; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 AA; 16081 MW; ECDBIA135E05B8AA CRC64;
                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0924R1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
                                                                                                                                                                                             PRT;
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                                                                                                                                                                                            PRELIMINARY;
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es 80; Conserv
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                        121 VSS 123
                                                                                                                    136 VSA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 VSS 123
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SEQUENCE
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61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGWYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                 Kozono Y., Kozono H., Azuma T.;
Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl) Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067781; BAB63266.1;
InterFro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.9%; Score 412; DB 11; Length 14
63.4%; Pred. No. 2e-35;
tive 19; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 AA; 16216 MW; 92460F1FDF1B7538 CRC64;
                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 AA.
                             01-DEC-2001 (TrEMBLrel. 19, Last sequent MAR-2002 (TrEMBLrel. 20, Last and VH186.2-D-J-C mu protein (Fragment).
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kozono Y., Kozono H., Azuma T.;

**Direct Estimation of Relative Affinity by Flow Cytometry Reveals

**Affinity Maturation of B Cell Antigen Receptors in Response to (4-

### Hydroxy-3-Nitrophenyl)Acetyl (NP).";

#### Rowsy-3-Nitrophenyl)Acetyl (NP).";

**EMBL; AB067794; BAB63279-1;

InterPro; IPR003006; I9_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                         Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.5%; Score 409.5; DB 11; Length 145; 63.2%; Pred. No. 3.7e-35; Live 17; Mismatches 22; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                         .
S
                                                                                                                                                                                                                                                                                                                                                                                            Score 411.5; DB 4; Length 116; Pred. No. 1.7e-35; 3; Mismatches 25; Indels 5
                                                                                                                                                                         Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 AA; 16011 MW; 9BC0846D40DF97EA CRC64;
                                                                                                                                                                                                                                                                                                                                                     116 116 116 116 AM; C8F9131DE13EA898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
                                                                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035025; AAD56261.1; -.
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00356; Ig_V.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                62.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 1.
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                                                                                                                             NCBI_TaxID=9606;
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SEQUENCE
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1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 6, 2003, 12:46:55; Search time 29.2727 Seconds (without alignments) 573.557 Million cell updates/sec Run on:

1 MRPSIQFLGLLLFWLHGAQC......YCLQYDNLWTFGGGTKLEIK 126 US-09-155-739-2 680 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 segs, 133250620 residues Searched: 908470 Potal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_101002:*

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| SIDS2/gcgdata/geneseq/geneseqp-emb1/Aa1981.DAT:*
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(\$1D82/goddata/geneseq/geneseqp-embl/AA2001.DAT:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Mouse VLA-4 antibo	Human VLA-4 reshap	Alpha-4 integrin m	MEI-14 light chain	Humanised alpha-4	Variable region of	Mouse anti-VLA-4 a	Human MCP-3 and mu	Human IP-10 and mu	Artificial synthet
	ID	AAR81326	AAR81332	AAW22409	AAR60627	AAW22419	AAR06252	AAR81328			
	Query Match Length DB ID	126 16	126 16	126 18	128 15	126 18	128 11	106 16		361 20	
dР	Query Match Le	100.0	100.0	100.0	93.2	91.0	91.0	83.7	79.3	79.3	78.7
	Score	680	680	680	634	619	618.5	569	539	539	535
	Result No.	-	7	9	₹	S	9	7	8	6	10

in va anti alph noclc TA fu	Antl-1954 wab ito SCF((FWF51). Synt R. piplens recombl Murine OKT4A light FWP51 fusion prote CD4-specific CDR-9 Ganqlioside GDR-9		3D3) ch eque 3D3 D23 111 L	acid acid acid IGFA immu bopoi prot
AAR78970 AAR81321 AAW22412 AAR93159 AAR26983	AAW26/9/ AAR85495 AAW35133 AAR13658 AAR13050 AAR13050	000000	AABB1997 AAR12359 AAX56724 AABB1993 AAW70379 AAR30880 AAW22842	W 2 4 2 4 2 4 2
16 118 113 113	77 77 77 77 77 77 77 77 77 77 77 77 77	18 23 22 15 17	12 12 12 13 14 14	222
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ALIGNMENTS

Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic; antibody engineering. 21..43 /note= "framework region 1" 44..54 /note= "complementarity determining region 1" 5 complementarity determining region 3" //note= "complementarity determining region 77..108 /note= "framework region 3" Mouse VLA-4 antibody 21.6 light chain variable region. /note= "framework region 4" /note= "framework region 2" /note= "signal peptide" Location/Qualifiers AAR81326 standard; Protein; 126 AA. 23-MAR-1996 (first entry) ..116 /note= "c 117..126 55..69 fus musculus. AAR81326; Peptide Region Region Region Region Region Region Region Key RESULT 1 AAR81326 Location/Qualifiers

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Query Match
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                                                                                                                                                                                                                                             The sequence represents the mouse antibody 21.6 light chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned CDNA sequences of mouse 21.6 V and VII (see AA099892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR Primers (See AA099895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, by the amino acid present in the equivalent position of the mouse 21.6 If Chain, Plasnids encoding the chimeric antibodies are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GKRPRLLIHYTSALQPGIPSRFSGSGGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic; antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                 21.6 Ig L chain. Placemids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies are to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, amoningitis or encephalitis. The antibodies can also be used for anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human VLA-4 reshaped antibody 21.6 light chain variable region.
                                                                                                                                                                             New humanised antibodies against VLA-4 - used for inhibiting legkocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 680; DB 16; Length 126; 100.0%; Pred. No. 2.1e-47; 1ve 0; Mismatches 0; Indels 0;
                                                                                                                   Bendig MM, Jones TS, Leger OJ, Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR81332 standard; Protein; 126 AA.
                                                                                                                                                                                                                           Disclosure; Fig 1; 105pp; English.
                                                                                            (ATHE-) ATHENA NEUROSCIENCES INC.
                                                95WO-US01219
                                                                      94US-0186269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity 100.0
Matches 126; Conservative
                                                                                                                                                                                                   inflammatory disease.
                                                                                                                                          WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 126 AA;
                                                                                                                                                     N-PSDB; AAQ99889
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                                                                    25-JAN-1994;
W09519790-A1
                                             25-JAN-1995;
                       27-JUL-1995
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chain variable region against leukocyte adheaion molecule VLA-4.

Cloned cDNA sequences of mouse 21.6 VL (AAQ99889) and VH (AAQ99892)

regions are linked to human constant regions in the construction
of a humanized antibody against VLA-4. The 5' and 3' ends of the
mouse CDNAs are modified using PCR primers (See AAQ9989-98) and
then subcloned into mammalian cell expression vectors containing
human kapa or gamma-1 constant regions. In the humanized light
chain, amino acids L45' L49' L58 and L69 in the human kapa LC VR
framework are replaced by the amino acid present in the equivalent
position of the mouse 21.6 IJ Lohain. Plasmids encoding the
conforthelial cell and to treat inflammatory diseases such as
multiple sclerosis. They can also be used in the treatment of
stroke, cerebral traumas, meninglits or encephalitis. The
antibodies can also be used for detecting VLA-4, for affinity
purification or for generating anti-idiotype antibodies.
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                                                                                                   "complementarity determining region 1"
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                                                                                                                                                                                                         "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leger OJ, Saldanha J;
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note= "framework region 3"
                                                  "framework region 1"
                                                                                                                                                      "framework region 2"
                                                                                                                                                                                                                                                                                                                                                            "framework region 4"
'note= "signal peptide"
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Homo sapiens.

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This polypeptide comprises the light chain variable region (VL) of mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VL can be incorporated into a human REI framework to produce a claimed
                                                                                                                                                                                    Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastias; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.

    for treatment of

                                                                                                                                                                                                                                                                                                                                                                                                        "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "complementarity determining region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma, atherosclerosis, AIDS, dementia, etc.
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                                                                                                                                                               Alpha-4 integrin mouse MAb 21.6 VL region.
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1..20
                                                                                     AAW22409 standard; Protein; 126 AA
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/label= CDR1
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/label- FR1
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/label= FR2
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N-PSDB; AAT74759.
               121 TKLEIK 126
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 121
                                                                         AAW22409
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61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
humanised 21.6 VL (see AAM22412) and a claimed humanised 21.6 antibody that is used in the manufacture of a medicament for treating a disease selected from asthma, atherosciarosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatord arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha 4 integrin for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibodies of the invention have a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of the MEI-14 light chain. The protein is monoclonal antibody which can be administered to treat solid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Method of treating solid or cystic tumours with antibodies administering monoclonal antibody Mel-14, having Fc deleted, using injection or deposition in the cyst cavity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 680; DB 18; 100.0%; Pred. No. 2.1e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ME1-14 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zalutsky MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR60627 standard; Protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-US02724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0033864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JUN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bigner DD, Carrel S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ZALUZ) ZALUTSKY M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-316669/39.
N-PSDB; AAQ73537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIGN/) BIGNER D D. CARRY) CARREL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cystic tumours.
See also AAR60626.
                                                                                                                                                                                                                                                                                                                                                                                                        126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TKLEIK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9421294-A.
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                                                                                                                                                                                                                                                                                                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR60627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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24-JAN-1990;
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                                               Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP380068-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR06252;
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
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                                                                                         GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                      Gaps
                                                          1 MRPSIQFLGLLEWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                              'note= "21.6 complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "21.6 complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "21.6 complementarity determining region 2"
                                                                                                                                                                                                                                  Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma: atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatory arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                     ö
                   Score 634; DB 15; Length 128;
Pred. No. 1e-43;
3; Mismatches 5; Indels (
                                                                                                                                                                                                                    Humanised alpha-4 integrin antibody 21.6 VL version La.
                                                                                                                                                                                                                                                                                                                                                       /label= Mat_protein
/note= "VL version La (Claim 25)"
                                                                                                                                                                                                                                                                                                                                                                                      'note= "REI framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= FR4
/note= "REI framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "REI framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                     "REI framework region 2"
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                       AAW22419 standard; Protein; 126 AA.
                                                                                                                                                                                                                                                                                                                                  1..20
/label= Leader
                    Query Match
Best Local Similarity 93.7%;
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               44..54
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                             70..76
/label- CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                      55..69
/label= FR2
                                                                                                                                                                                                                                                                                                                                                                                /label= FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FR3
                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77..108
/label=
                                                                                                                                                                                                                                                                                                                                               21..126
                                                                                                                                                                                                                                                                                                                                                                                                                                       note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note=
                                                                                                                                                                                                                                                                                         Chimeric Mus musculus;
                                                                                                                                                                                                                                                                                                  Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                        Chimeric synthetic.
     128 AA;
                                                                                                                121 TKLEIK 126
                                                                                                                               121 TKLEIK 126
                                                                                                                                                                                                      08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9718838-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAY-1997
     Sequence
                    Query Match
                                                                                                                                                                                      AAW22419;
                             Best Local
                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                Protein
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This polypeptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also AMM22412). It is composed of complementarity determining regions from the VL region (see AMM2240) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human REI framework. It can be expressed in mammalian host cells following PCR amplification and munanised 21.6 VL and a humanised 21.6 VH (see AMM22413) can be used to produce a claimed humanised 21.6 antibody that is useful in the manufacture of a medicament for treating asthma, atherosofaciosis, arthritis, diabetes, inflammatory bowel disease, theumatoid arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, archiology dermatitis, psoriasis, myocardial cantibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRPSIQFLGLILFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                            Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
91.0%; Score 619; DB 18; Length 126;
Best Local Similarity 90.5%; Pred. No. 1.6e-42;
Matches 114; Conservative 6; Mismatches 6; Indels (
                                                                                                                                                                                                            Leger OJ, Saldanha J, Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Variable region of murine AHT 107 light chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Fig 10; 107pp; English.
                                                                                                                                      (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                      95US-0561521,
   96WO-US18807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90EP-0101351.
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                                                                                                                                                                                                         Jones ST,
                                                                                                                                                                                                                                                                         WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 126 AA;
                                                                                                                                                                                                                                                                                                            N-PSDB; AAT74788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TKVEIK 126
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21-NOV-1996;
                                                                      21-NOV-1995;
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Human MCP-3 and murine scFv38 fusion protein.
                                                                                                                                            25-JAN-1994;
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                                                                                        WO9519790-A1
                                                                                                                          25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY29913;
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         Region
                                           Region
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ID AAY2
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AC AAY2
XX
DT 17-N
XX
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1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTLTCKTSQDINKFIAWYQHKP 60
                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                            1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                          MADS comprising mouse CH and CL constant regions whith human variable regions may be used to create mouse/human hybrid MADS, which have a longer serum half-life. Method can be used to produce ADS against interleukin-2 receptor and tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "mouse light chain variable complementarity
determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "mouse light chain variable complementarity determining region 2"
                                                                             Expression vectors for producing chimeric monoclonal antibodies - which express human constant region and non-human variable region
                                                                                                                                                                                        91.0%; Score 618.5; DB 11; Length 128; 88.2%; Pred. No. 1.8e-42; Live 12; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "mouse light chain variable framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "mouse light chain variable framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note- "mouse light chain variable framework
                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse anti-VLA-4 antibody 21.6 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                AAR81328 standard; Protein; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region 1ª
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50..56
/label- CDR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= FR1
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89US-0301216
                  (MOLE-) MOLECULAR THERAPEU.
                                                                                                                                                                                                                                                                                                                                                                                                    02-APR-1996 (first entry)
                                                                                                                                                                                                            Matches 112; Conservative
                                                                                                          Disclosure; ; p; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35..49
                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody engineering.
                                                     WPI; 1990-232892/31
                                                                                                                                                                                                  Sest Local Similarity
                                                                                                                                                                         128 AA;
                                                                                                                                                                                                                                                                                                             |||||::
121 GTKLEVR 127
                                                                                                                                                                                                                                                                                                   120 GTKLEIK 126
                                                             N-PSDB; AAQ05556
24-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                   AAR81328;
                                     Zerler B;
                                                                                                                                                                         Sequence
                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Region
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The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain variable region (without signal sequence). Cloned cDNA CDR sequences of mouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the REI antibody for the light chain and the 2*CL antibody for the heavy chain in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AA09895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LCVR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig light chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukcoyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephaltiis. The antibodies can also be used for detecting VM-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQWIQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 60
                                                                                                     /note= "mouse light chain variable complementarity
determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                       /note= "mouse light chain variable framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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100.0%; Pred. No. 1.4e-38;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bendig MM, Jones TS, Leger OJ, Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 66; 105pp; English.
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region 3"
                                                                                                                                                                                                                                                                               region 4"
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                                89..96
/label= CDR3
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Matches 106; Conservative
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The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human interferon-fuduced protein 10 (IP-10) and human Muc-1; (4) human SPF-1 and human Muc-1; (5) human IP-10 and HIV gpl20; (6) human MCP-3 and HIV gpl20; (7) human MDC and HIV gpl20; and (8) human SPF-1 and HIV gpl20; The fusion proteins, and nucleotide sequences encoding them, can be used for producing an immune response, e.g. an effector T cell immune response. They can also be used for treating cancer or treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences for identifying unknown tumour antigen epitopes and fine mapping of them in without antigen epitopes and fine mapping of them in which is the contact the contact antigen and fine mapping of the company of the contact antigen and the mapping of the contact antigen and the mapping of the contact antigen antigen and the mapping of the contact and the contac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour antigen epitopes. The present sequence represents a fusion protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
                            Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine; immune response; HIV; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human IP-10 and murine scFv38 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 118-119; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 91.8 Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kwak LW, Biragyn A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-551418/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 AA;
                                                                                                             Homo sapiens
                                                                                                                                                                                                                     W09946392-A1
                                                                                                                                                                                                                                                                                                                                12-MAR-1999;
                                                                                                                                                                                                                                                                            16-SEP-1999.
                            Chemokine;
                                                                                                                                          Mus sp.
Synthetic.
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The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen. Specifically claimed fusion proteins (Comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human SDF-1 and human Muc-1; (5) human IP-10 and HIV gpl20; (6) human MCP-3 and HIV gpl20; (7) human MCC and HIV gpl20; and (8) human SDF-1 and HIV gpl20. The fusion proteins, and nucleotide sequences encoding them, can be used for producing an immune response. G.g. an effector T cell immune response. They can also be used for treating cancer or treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays tumour antigen epitopes. The present sequence represents a fusion protein has nreash; invention
                                                                                                                                                                                                                                                                           New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine; immune response; HIV; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 539; DB 20; Length 361; Pred. No. 1.2e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 GIPSRESGSGSGRDYSFSISNLEPEDIATYCLQYDNLYTFGGGTKLEIK 340
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                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 115-116; 142pp; English.
                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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91.8%;
                                                                                                                                                98US-0077745
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 AA;
                                             WO9946392-A1
                                                                                                               12-MAR-1999;
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                                                                              16-SEP-1999,
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Mus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                            infection
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                                                                                                                                                                                                                                                                                                New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 78.7%; Score 535; DB 20; Length 374; Best Local Similarity 94.3%; Pred. No. 2.6e-35; Matches 100; Conservative 3; Mismatches 3; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Light chain variable region for monoclonal antibody 23F8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLEIK 200
                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 117-118; 142pp; English.
                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                                                             Kwak LW, Biragyn A;
                                                                                                                                                                                                                                        WPI; 1999-551418/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JAN-1994;
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   12-MAR-1999;
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Hybridoma antibodies have been produced with the spleen cells of BALB/c mouse that had received multiple injections of mercuric ions reacted with glutathione to produce a mercuric ion coordinate covalent compound which was covalently bound to keyhole limpet hemocyanin (KLH). Eight hybridomas (IFIO, 4A10, ICII, SG4, 2878, 2D5, 5D6 and 3E8) were producing MAbs that were strongly positive spainst glutatione-mercuric ions but negative against glutathione without mercuric ions. RNA was isolated from hybridoma cells with quanidine isothiocyanate. First strand cDNA synthesis was catalysed by Mulv reverse transcriptase. The primers used for cDNA synthesis of the chain expressed by the hybridoma of interest, or to the 5' and of the C kappa domain. Some of the primer used for cDNA synthesis are shown in AA097511-097518. The primer used for cDNA synthesis of the crimiale region of a particular antibody polypeptide was also used for PCR amplification of that variable region, in conjunction with an appropriate V-region primer. In addition, the VH primer AA097518 was used to amplify the mAb 2D5 and 5D6 heavy chains. The sequences of the PCR amplified nucleotides were determined. These are given on hand a handoy180-0878071. The descriptions of the SEQ ID nos given on pp 44-45 and in the claims are different from the descriptions in the sequence listings are
                                                                                                                                                        New polypeptide(s) which bind heavy metals, esp. mercury - derived from monoclonal antibodies, used for detecting, removing, adding or neutralising heavy metals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 75.1%; Score 510.5; DB 16; Length 107; 1 Similarity 91.6%; Pred. No. 7e-34; 98; Conservative 3; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 23; Page 67-68; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR81321 standard; Protein; 106 AA
   Wylie DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-US01219.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody engineering.
Lopez O, Wagner FW,
                                                                      WPI; 1995-275415/36.
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Best Local Similarity
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                                                                                                             N-PSDB; AAQ97508
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Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma: atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                               New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                             81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised alpha-4 integrin antibody 21.6 VL La.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW22412 standard; Protein; 106 AA
                                          Leger OJ,
                                                                                                                      Claim 9; Page 67; 105pp; English.
                     (ATHE-) ATHENA NEUROSCIENCES INC
 94US-0186269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 88.7 les 94; Conservative
                                       Bendig MM, Jones TS,
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Chimeric Homo sapiens;
Chimeric synthetic.
                                                                                                      nflammatory disease
                                                             WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                                                                             106 AA;
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AAW22412
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This polypeptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human REI framework. It can be expressed in mammallan host cells following PCR amplification and mutagenesis of appropriate fragments of mouse and human DNA sequences. The humanised 21.6 VL and a humanised 21.6 vM (see AAW22413) can be used to produce a claimed humanised 21.6 antibody that is useful in the manufacture of a medicament for treating asthma, atherosclerosis,
                                                                 /note= "21.6 complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "21.6 complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "REI Val-58 is substd. by Ile of mouse 21.6 VL, important in supporting the CDR2 loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "21.6 complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "REI Leu-103 substd. by Val, more typical of human kappa light chain J region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "REI Gln-104 substd. by Glu, more typical of human kappa light chain J region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "REI Thr-106 substd. by Lys, more typical of human kappa light chain J region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                             /note= "REI Lys-45 is substd. by Lys of mouse
21.6 VL, important in supporting the
CDR2 loop"
                                                                                                                                                                                                                                                                                                                                          /note= "REI Tyr-49 is substd. by His of mouse 21.6 VL, located at the binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "REI Thr-69 is substd. by Arg of mouse 21.6 VL, involved in antibody-antigen binding"
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                                                                                                                                                            /note= "REI framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "REI framework region 3"
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   24..34
/label= CDR1
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/label= CDR2
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/label= FR4
                                                                                           35..49
/label- FR2
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/label- FR3
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                                                                                                                                                                                          Misc-difference 45
                                                                                                                                                                                                                                                                                                               Misc-difference 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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      Region
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                                                                                                               Saldanha J;
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AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid

/note= "REI framework region 1"

/label= FR1

Location/Qualifiers

Key Region

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81
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                                                                                                                                       21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                               Antibody; light chain; kappa; variable region; K20; integrin; CD29; beta 1 subunit; humanisation; Hu-K20; immunosuppressant; T cell activation; complementarity determining region; CDR.
                     The antibody
arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
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                                                                                                 Score 508; DB 18; Length 106;
Pred. No. 1.1e-33;
6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "complementarity determining region" 95..108
                                                                                                                                                                                                                                                                                                 Murine monoclonal antibody K20 kappa chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                              "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "complementarity determining region"
                                                                                                                                                                           81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                      (INRM ) INSERM INST NAT SANTE & RECH MEDICALE. (PROT-) PROTEINE PERFORMANCE SA.
                                                                                                                                                                                                                                                                                                                                                                                                  /note= "framework region"
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                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/label= J_kappal
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                                                                                                   74.7%;
ilarity 88.7%;
Conservative 6
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/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                            14..34
| Tabel = CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94FR-0010858
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/label= FR2
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/label= FR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          "note=
                                                                                                             Local Similarity
                                                                                   Sequence 106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-1996.
                                                                                                                       94;
                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                       The present sequence is that of the variable region of the kappa light chain from murine monoclonal antibody K20. The antibody recognises the beta I subunit (CD29) of integrins and inhibits activation and proliferation of peripheral T cells induced by anti-cD3 antibodies. Monoclonal antibody K20 is a preferred target for humanisation; the humanised version may be useful as an immunosuppressant. In the humanisation process, the complementarity determining regions (CDKS) of a human antibody with framework regions 70-95% homologous to those of K20 were replaced by the K20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12..29
/label- FLAG_peptide_and_enterokinase_cleavage_site
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                                                                                                                                               Humanisation of non-human immunoglobulin variable regions - for prodn. of humanised antibodies, esp. K20, e.g. as an immunosuppressant
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/label= FRP5_light_chain_variable_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYYNLWTFGGGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
Cervoni MF, Lefranc MP, Margaritte C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.7%; Score 508; DB 17;
89.6%; Pred. No. 1.1e-33;
tive 5; Mismatches 6;
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/label= ETA_252-613
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                                                                                                                                                                                                                                                              Example 1; Fig 2A; 39pp; French
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Matches 95; Conservative
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                                                                          WPI; 1996-162083/17
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  Bernard A,
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                           Poul MA;
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The sequences given in AAR26982-3 contain part of the exotoxin A sequence corresponding to positions 252-613 of the full exotoxin A sequence. These sequences are encoded by FV(FRE)-FTA fusion genes. The ETA sequence was used as a marker gene so that E. coli transformed expressed in E. coli and the antibodies were extracted. These recombinant antibodies can be used for the qualitative and quantitative determination of c-erbB-2. This can be used for monitoring or in-vivo localisation of tumours overexpressing c-erbB-2.
                                                                                                                                                               Recombinant antibodies directed to growth factor receptor C-erbB-2 for diagnosing and treating tumours expressing C-erbB-2 e.g. breast
                                                                   Harwerth I, Hynes NE, Wels WS;
                                                                                                                                                                                                                            Disclosure; Page 53-58; 67pp; English.
   91EP-0810079.
                                (CIBA ) CIBA GEIGY AG.
                                                                   Hardman N,
                                                                                                              WPI; 1992-302096/37.
                                                                                                                                                                                                  or ovarian tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                637 AA;
                                                                                                                                  N-PSDB; AAQ28263.
05-FEB-1991;
                                                                 Groner B,
Zwickl M;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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; 0 Gaps 17 GAQCDIQMTQSPSSLSASLGGKVTLTCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76 ö Query Match 74.7%; Score 508; DB 13; Length 637; Best Local Similarity 86.4%; Pred. No. 6.4e-33; Matches 95; Conservative 5; Mismatches 10; Indels 77 GIPSRFSGSGGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126 g ò

Search completed: January 6, 2003, 13:15:15 Job time : 31.2727 secs

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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: January 6, 2003, 13:13:21; Search time 10.4364 Seconds (without alignments)
355.228 Million cell updates/sec 680
Sequence: 080
Sequence: 080
Scoring table: BLOSUM62
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Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
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7: /cgn2_6/ptodata/1/laa/pctitles1.pep:*
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query Match
100.0%; Score 680; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.7e-59;
Matches 126; Conservative 0; Mismatches 0; Indels (

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		1 1 -561-521-2 ent No. 5840299 NERAL INFORMATION: APPLICANT: Bendig, Mary M. APPLICANT: Bendig, Mary M. APPLICANT: Bendig, Mary M. APPLICANT: Bendig, Mary M. APPLICANT: Baldanha, Jose APPLICANT: Saldanha, Jose APPLICANT: Jose APPLICANT: Jose APPLICANT: Saldanha, Jose TITLE OF INVENTION: Humanized Ant TITLE OF INVENTION: Adhesion Mole WINNERS OF SEQUENCES: 45 CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsen STREET: One Market Plaza, Steua CITY: San Francisco STREET: One Market Plaza, Steua COUNTRY: USA ILIY: San Francisco STATE: California COUNTRER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PLOCATION DATA: APPLICATION NUMBER: US/08/561,5 FILING DATE: CLASSIFICATION NUMBER: US/08/186,2 FILING DATE: CLASSIFICATION NUMBER: US/08/186,2 FILING DATE: 25-JAN-1994 ATTORNEY AGENT INFORMATION: REGISTRATION NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 30,223 REFERENCE/DAMINICATION INFORMATION: TELEFRAX: 415-543-960
22 22 22 22 22 22 22 23 23 23 24 25 25 25 25 25 25 25 25 25 25 25 25 25		2 Septication US/08E 840299 ORMATION: Bendig, Mary M.: Bendig, Mary M.: Leger, Olivier: Leger, Olivier: Lager, Olivier: Lones, S. Tarra Invention: Humani Invention: Humani Invention: Adhess; S. Tarra Invention: Adhess; S. Tarra Invention: Adhess; A 5 Septiment of the Market Plaza San Francisco California Gone Market Plaza San Francisco California Gone Market Plaza San Francisco California EE: Townsend and One Market Plaza San Francisco California EP Patentin Relegible EP Patentin NUMBER: US/UICATION NUMBER: US/UICATION NUMBER: 30 CALS MAITON NUMBER: 30 CAL
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APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Overy Match 100.0%; Score 680; DB 2; Length 126; Best Local Similarity 100.0%; Pred. No. 1.7e-59; Aqtches 126; Conservative 0; Mismatches 0; Indels
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California
                                                                                                                                                                                                                                                                                                                                                                                           Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15270-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/561,52;
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                                                                                                                                                                                                                       Sequence 15, Application US/08561521
Patent No. 5840299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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INFORMATION FOR SEQ ID NO: 15:
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ADDRESSE: Townsend &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94105
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US-08-561-521-15
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1 MRPSIQFLGLLEWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
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APPLICANT: Beger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 126;
                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 680; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.7e-59;
Matches 126; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTATION NUMBER: 30,223
REPERBNCE/DOCKET NUMBER: 15270-14
TELECOMUNICATION INFORMATION:
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GENERAL INFORMATION:
Sequence 2, Application PC/TUS9501219 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Leger, Olivier J.
Saldanha, Jose
Jones, S. Tarran
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                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
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; MOLECULE TYPE: protein
PCT-US95-01219-2
                                                                                                                                                                                                                      STREET: One Market P
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC OPERATING SYSTEM:
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PCT-US95-01219-15
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APPLICANT:
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APPLICANT:
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linear
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TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS:
                                                                                      ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08339582;
Patent No. 5558852;
GENERAL INFORMATION:
APPLICANT: Bigner, Darell D.
APPLICANT: Zalutsky, Michael R.
APPLICANT: Carrel, Stefan
TITLE OF INVENTION: METHOD OF TREATMENT;
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 15270-14
                                                                                                                                                                                                                                                       COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: NO. 555885zth Carolina
COUNTRY: USA
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TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
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                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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; MOLECULE TYPE: protein
PCT-US95-01219-15
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                                                                                                                               CITY: San Francisco
STATE: California
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CLASSIFICATION:
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                                                                                                                                                                         COUNTRY:
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61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
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APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.2%; Score 634; DB 1; Length 128; Best Local Similarity 93.7%; Pred. No. 5.4e-55; Matches 118; Conservative 3; Mismatches 5; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                           FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,864
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-89
TELECHONE: 919-420-2200
TELECHONE: 919-881-3175
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acids
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                                                                                                           APPLICATION NUMBER: US/08/339,582
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08561521; Sequence 5, Application US/08561521; Patent No. 5840299; GENERAL INFORMATION: APPLICANT: Bendig, Mary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-339-582-4
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California
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Sequence 22, Application US/08888366
Patent No. 5972656
GENERAL INFORMATION:
APPLICANT: Mylie, Dwane E.
APPLICANT: Walle, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefo
                                                                                              0; Gaps
                                                                                                                                                   1 DIQMTOSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 60
                                                                                                                            21 DIQMIQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
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                                                83.7%; Score 569; DB 5; Length 106; 100.0%; Pred. No. 9.8e-49; Live 0; Mismatches 0; Indels
                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                        81 RFSGSGSGRDYSFNISNLEPEDIATYYCLOYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-2AN-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
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TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: LENGTH: 107 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Carter, Charles G. REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                        Conservative
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                                                                   Best_Local Similarity
Matches 106; Conserv
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US-08-888-366-22
          PCT-US95-01219-5
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                                                  Query Match
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APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   83.7%; Score 569; DB 2; Length 106; 100.0%; Pred. No. 9.8e-49; tive 0; Mismatches 0; Indels
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CITY: San Francisco
STATE: California
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          NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REPERRECE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER: PCT/US95/01219
25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/POCKET NUMBER: 15,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFRAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NFORMATION FOR SEQ ID NO: 5:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 106 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94105
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STATE:
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1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF EVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.7%; Score 508; DB 2; Length 106; 88.7%; Pred. No. 9e-43;
                                                                   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGGGTKLEIK 126
                                                                                              81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECHONE: 415-543-9600
TELEFRAN: 415-543-9600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 88.79
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                    TITLE OF INVENTION. Humanized Antibodies Against Leukocyte TITLE OF INVENTION. Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.7%; Score 508; DB 5; Length 106; 88.7%; Pred. No. 9e-43; tive 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Hynes, Nancy E.
APPLICANT: Hynewerth, Ina Maria
APPLICANT: Hardman, No. 5571894man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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                                                                                                                                                                              E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/01219 FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Smith, William L. REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/08235838 Patent No. 5571894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
Leger, Olivier J.
                           Saldanha, Jose
Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 106 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.78
Matches 94; Conservative
                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                     COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-235-838-16
                                                                                                                                                                                                      STREET:
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New York

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TELEFAX: (908)522 6955
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wels, Winfried S. APPLICANT: Hynes, Nancy E.
       FILING DATE: 5 June 1995
                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-465-473B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INPORMATION:
APPLICANT: Wals, Winfried S.
APPLICANT: Harwes, Nancy E.
APPLICANT: Harwes, Nancy E.
APPLICANT: Harwes, Nancy E.
APPLICANT: Groner, Bernd
APPLICANT: Ardnen, No. 5939531man
APPLICANT: Zwickl, Markus
ITILE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS COIPORTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLOYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.7%; Score 508; DB 1; Length 637; 86.4%; Pred. No. 7.5e-42; Live 5; Mismatches 10; Indels
                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,838
FILING DATE: TBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
                                                                                                                                                                                                                     CLASSIFCATION: 435

CLASSIFCATION: DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 31-302
PRIOR APPLICATION DATA:
APPLICATION WHEBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REGISTRATION NUMBER: 4-18518/A/CIP/CONT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ. 10 NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/08465473B Patent No. 5939531
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 637 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 86.49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                    MEDIUM TYPE:
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US-08-465-473B-16
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH:
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Matches
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17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
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APPLICANT: Groner, Bernd
APPLICANT: Groner, No. 5571894man
APPLICANT: Zwickl, Markus
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 16
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
SURREWI APPLICATION DATA:
APPLICATION NUMBER: US/08/235,838
FILING DATE: TBA
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-AN-1992
PRIOR APPLICATION DATA:
FILING DATE: 31-AN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,932
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 91-810079.3
                                                                                                                                                                                         NAME: Pfelffer, Hesna J.
REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 7 Skyline Drive CITY: Hawthorne STATE: New York COUNTR: USA
                                                                                                                GB 91-810079.3
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08235838
Patent No. 5571894
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5939531man
APPLICANT: Arickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS Corporation
STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                              Query Match 74.0%; Score 503; DB 1; Length 241; Best Local Similarity 86.2%; Pred. No. 7.3e-42; Matches 94; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 GIPSRESGSGSCRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
FILING DATE: 5 June 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Pfeiffer, Hesna J.

REGISTRATION NUMBER: 22,640

REECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940

TELEPHONE: (908)522 695

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                     4-18518/A/CIP/CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB 91-810079.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08465473B Patent No. 5939531 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-185
TELECOMMUNICATION INFORMATION:
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 annino acids
TYPE: annino acids
TYPE: annino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 05-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 amino acids
                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-235-838-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901-6940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-08-465-473B-11
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245 GGGSDIQMTQSPSSLSASLGGKVTITCKASQDIKKSIAWYQHKPGKGPRLLIHYTSTLQP 304
                                                                                                                                           0; Gaps
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                                                                                                                                                                                17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
                                                                                                   Length 241;
                                                                                                                                                                                                                                                                                          193 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241
                                                                                                                                                                                                                                                                  77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEI 125
                                                                                                Score 503; DB 2; Length 24:
Pred. No. 7.3e-42;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Liuis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 501; DB 3;
Pred. No. 1.8e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 015280-244100US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCI/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/011,800
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 57, Application US/08875811 Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.78;
86.48;
                                                                                                   74.0%;
86.2%;
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 57
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 amino acids
                                                                                        Query Match
Best Local Similarity 86.27
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 73.77
Best Local Similarity 86.4*
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Faris, Susan K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-875-811-57
               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       California
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
  ; TYPE: aminc; TOPOLOGY: ]; MOLECULE TYPE: US-08-465-473B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-08-875-811-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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Search completed: January 6, 2003, 13:19:07 Job time: 11.4364 secs

According to the Pre Publication Rules, every patent application received by the United States Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the sequences, will become prior art.

Two new databases have been created to hold the pre-published sequences:

Published_Applications_NA contains nucleic acid sequences; the search results will have the

Published_Applications_AA contains amino acid sequences; the search results will have the

Each pre-published application is given a unique Publication Number. An example of a Publication Number is US20021234567A1. The "US" indicates the application was a U.S. application. The first 4 digits show the calendar year the application was published. The next 7 digits represent when the application was published. This 7-digit number starts at zero at the beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the application had been published. If the applicants submit changes to the application, they may requests that the changed application be published again. In such instances, the "1" at the end of the number would be replaced by a "2".

Sequences in the PGPub database are public information; it is permissible to leave these

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January 6, 2003, 13:17:36; Search time 6.10909 Seconds (without alignments) 390.875 Million cell updates/sec
                                                                                                                                                                                                                                                                                                1 MRPSIQFLGLLLFWLHGAQC......YCLQYDNLWTFGGGTKLEIK 126
                            Compugen Ltd.
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                         117078 seqs, 18951520 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                 OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
                                                                                                                                                                                                                                                                            Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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14: /cgn2_6/ptodata/2/pubpaa/USOZ_PUBCOMB.pep:*

Published_Applications_AA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2, Appli 4, Appli 26, Appl 1, Appli Sequence 30, Appl Sequence 21, Appl Sequence 24, Sequence 11, Sequence 15, Sequence 16, Sequence 10 Sequence 17 Sednence 1 Sequence Seq Description Sequence Sequence Sequence Sequence 0 US-08-79-784-21 0 US-08-779-784-21 0 US-09-740-002-24 0 US-09-764-304-10 0 US-09-229-200A-11 0 US-09-229-200A-15 0 US-09-229-200A-16 0 US-09-800-729-150 0 US-09-800-729-150 0 US-09-800-729-150 0 US-09-800-729-150 0 US-09-800-729-150 0 US-09-800-729-150 0 US-09-140-02-26 0 US-09-740-02-26 0 US-09-740-02-26 0 US-09-740-02-26 0 US-09-739-1 0 US-09-10-739-1 0 US-09-10-739-1 0 US-09-10-739-1 0 US-09-10-739-1 US-09-229-200A-7 US-09-229-200A-17 US-09-859-053-30 Query Match Length DB Score 416 414.5 413.5 435.5 434.5 434.5 431.5 431.5 420.5 418.5 418.5 Result ş

20 407.5 59.9 107 10 US-09-056-160B-15 21 405 59.9 235 10 US-09-00-166-6 22 405 59.6 237 10 US-09-056-160B-103 24 403.5 59.3 107 10 US-09-056-160B-103 24 403.5 59.2 108 10 US-09-056-160B-103 26 402.5 59.2 108 10 US-09-081-123-6 27 401.5 59.0 127 10 US-09-081-123-6 29 401.5 59.0 127 10 US-09-056-160B-105 29 401.5 59.0 127 10 US-09-056-160B-105 30 400.5 58.9 108 9 US-10-153-159-1 31 400.5 58.9 108 10 US-09-056-160B-107 31 397.5 58.5 10 US-09-056-160B-117 32 397.5 58.5 10 US-09-056-160B-117	Sequence 15, Appl Sequence 6, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 15, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appli Sequence 2, Appli
0.000000000000000000000000000000000000	US-09-056-160B-15 US-09-800-722-152 US-09-800-722-152 US-09-056-160B-133 US-09-056-160B-133 US-09-056-160B-105 US-09-056-160B-105 US-09-056-160B-105 US-10-153-159-16 US-09-056-160B-8 US-09-056-160B-8 US-09-056-160B-117 US-09-056-160B-117 US-09-056-160B-117 US-09-056-160B-117 US-09-056-160B-117 US-09-113-159-16 US-09-056-160B-117 US-09-113-159-16 US-09-166A-2 US-09-166A-2 US-09-166A-2 US-09-166A-1
0.000000000000000000000000000000000000	100 100 100 100 100 100 100 100 100 100
	107 235 235 237 110 110 110 110 110 110 110 110 110 11
20 407.5 21 22 24 404.05 25 26 4003.5 26 4003.5 27 4003.5 28 4001.5 300	0.000000000000000000000000000000000000
	0.04 0.04

ALIGNMENTS

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COUNTRY: USA
ZIP: 08933-7003
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                               APPLICANT: Jolliffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                    STREET: One Johnson & Johnson Plaza CITY: New Brunswick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: JOHN W. WALLEN, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
TELECOMUNICATION INFORMATION:
TELEPHONE: (858) 784-3239
TELEFAX: (908) 524-2808
INFORMATION FOR SEG ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 13-Jan-1999
CLASSIFICATION: <Unknown>
                                      Sequence 7, Application US/09229200A Patent No. US20020099179A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM
                      US-09-229-200A-7
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RESULT 1
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Gaps

5

Indels

72.1%; Score 490; DB 10; ilarity 86.1%; Pred. No. 8.8e-34; Conservative 8; Mismatches 5;

Query Match Best Local Similarity Matches 93; Conservat

Length 109;

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TELEFAX:
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APPLICANT: Tezuka, Katsunari
AITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTINULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 DIOMTOSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.0%; Score 482.5; DB 10; Length 108; 87.9%; Pred. No. 3.6e-33; rative 3; Mismatches 9; Indels 1;
                                                                                 81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW--TFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                 APPLICANT: JOILIFFE et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
STREET: One Johnson & Johnson Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 08933-7003
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                      61 RFSGSGSGRDYSFSISNLEPEDIATYCLQQYDNLLFFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
FILING DATE: 13-Jan-1999
CLASSIFICATION: <UDKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: John W. Wallen, III
RECISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 784-3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 17
                                                                                                                                                                                                                       Sequence 17, Application US/09229200A Patent No. US20020099179A1 GENERAL INFORMATION:
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TELEFAX: (908) 524 2808
INFORMATION FOR SEC ID NO: 17
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30, Application US/09859053
Patent No. US20020102658A1
GENERAL INFORMATION:
APPLICANT: Tsuji, Takashi
                                                                                                                                                                                                                                                                                                                                                                                                              New Brunswick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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Best Local Similarity 87.99
Matches 94; Conservative
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US-09-229-200A-17
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61 GKRPRLLIHYTSALQPGIPSRFSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: MILLER, DAVIDENTION: REVOUS SYSTEM
TITLE OF INVENTION: REVELINATION USING MONOCLONAL AUTOANTIBODIES
OORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                           65.1%; Score 442.5; DB 10; Length 236; 64.6%; Pred. No. 1.4e-29; tive 20; Mismatches 24; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR PPLICATION NUMBER: JP 2001-99508
PRIOR PLICATION NUMBER: JP 2000-147116
PRIOR PLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTHARE: PASISEQ for Windows Version 4.0
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ATTORNEY/ABORN INFORMATION:
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FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
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REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26,742
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 64.68.
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201-343-1684
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                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-09-859-053-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Jersey
: USA
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                                                                                                                                                                                                          SEQ ID NO 30
LENGTH: 236
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US-08-779-784-21
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US-09-764-304-19
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APPLICANT: BRAMS, PETER
APPLICANT: BRAMS, PETER
APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: MEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                                                                                                                                   1; Gaps
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                                                                                                                                                                                                                     1; Gaps
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                                                                                                                                    Length 131;
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                                                                                                                                / Match 64.3%; Score 437.5; DB 1;
Local Similarity 67.7%; Pred. No. 2e-29;
hes 86; Conservative 12; Mismatches 28;
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64.6%; Pred. No. 5.2e-29;
tive 14; Mismatches 30
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Patent No. US20020026036A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/09740002 Patent No. US20020001798A1
INFORMATION FOR SEQ ID NO: 21:
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amino acid
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               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SHITARA, KENYA
                                                                          , MOLECULE TYPE: protein US-08-779-784-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-09-740-002-24
                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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US-09-764-304-10
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LENGTH: 234
                                     LENGIH:
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                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                  APPLICANT: Jolliffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSES: Johnson & Johnson
STREET: One Johnson & Johnson
CITY: New Brunswick
                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 08933-7003
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETIE, 3.5 INCH, 1.44 Mb STORAGE
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GENERAL INFORMATION:
APPLICANT: JOLILIFFE et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
                                                                         61 RFSGSGSGTDYTFTISSLQPEDIATYXCQQYDNLIFTFGQGTKLQ1 106
                                                    81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEI 125
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APPLICATION NUMBER: US/09/229,200A
FILING DATE: 13-Jan-1999
CLASSIFICATION: CURNOWN>
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CITY: New Brunswick
STATE: NJ
COUNTRY: USA
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NAME: John W. Wallen, III
REGISTRATION NUMBER: 35,403
                                                                                                                                                                                                       Sequence 15, Application US/09229200A Patent No. US20020099179A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 784-3239
TELEFAX: (908) 524-2808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-229-200A-16; Sequence 16, Application US/09229200A; Patent No. US20020099179A1
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OPERATING SYSTEM: PC-DOS
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 108
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                                                                                                                                                                                                                                                                                                                                                  1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
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63.5%; Score 431.5; DB 10; Length 108;
Best Local Similarity 76.4%; Pred. No. 5.2e-29;
Matches 81; Conservative 11; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: JOILIFFE et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Johnson & Johnson
STREET: One Johnson & Johnson Plaza
CITY: New Brunswick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMDUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: -UNKNOWN>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: John W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (858) 784-3239
TELEFAX: (908) 524-2808
                                                                                                                                                OTHER INFORMATION: light chain OTHER INFORMATION: variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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SEQUENCE CHARACTERISTICS:
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                         Local Similarity 66.9% les 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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08933-7003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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US-09-229-200A-11
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                             SEQ ID NO 19
                                                                                                                                                                                           US-09-764-304-19
                                                                                                                                                                                                                                         Query Match
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Matches
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61.5%; Score 418.5; DB 10; Length
Best Local Similarity 63.0%; Pred. No. 7.8e-28;
Matches 80; Conservative 17; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                             Foon, Kenneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: WORINE ANTI-IDIOTYPE ANTIBODY 341
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 304142000102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/361,772
FILING DATE: 27-UL-1999
APPLICATION NUMBER: US 08/579,940
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/365,484
FILING DATE: 28-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/797,481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-797-481-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MORRISON & FOERSTER STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-Feb-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                    APPLICANT: Chatterjee, Malaya
Kohler, Heinz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 142 amino acids
                                                                                                                                                                                                                            Sequence 2, Application US/09797481 Patent No. US20010047083A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 GTKLEIK 126
                                                                       120 GTKLEIK 126
                                                                                                                   121 GTKVEIK 127
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                                                                                                                                                                                      RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GKRPRLLIHYTSALQPGIPSRFSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRVPAQLIGLILLWLSGARCDIQLTQSPSSLSASLGDSVTITCQASQDIANYLNWYQQKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIOMTOSPSSLSASVGDRVTITCKASPDINNYIAWYQHTPGKAPKLLIHYTSTLQPGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 63.5%; Score 431.5; DB 10; Length 108; Local Similarity 77.4%; Pred. No. 5.2e-29; les 82; Conservative 10; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30; Indels
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGTDYTFTISSLQPEDIATYCLQQYDNLIFTFGQGTKLQI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.8%; Score 420.5; DB 1
63.8%; Pred. No. 8.7e-28;
tive 15; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
                                                                                                                                                                  APPLICATION NUMBER: US/09/229,200A FILING DATE: 13-Jan-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                      NAME: JOHN W. WALLER, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 784-3239
TELEFAX: (908) 524-2808
INFORMATION FOR SEQ ID NO: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 150, Application US/09800729
Patent No. US20020068319A1
GENERAL INFORMATION:
                                                                          COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                          SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 63.8
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
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US-09-800-729-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-229-200A-16
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LENGTH: 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                              TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GKRPRLLIHYTSALQPGIPSRFSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRPSIQFIGLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 LLIHYTSALQPGIPSRFSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 QFLGLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bodmer, Mark W
APPLICANT: Activation:
APPLICANT: Activation:
APPLICANT: Activation:
APPLICANT: Activation:
APPLICANT: Activation:
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
FILE REFERENCE: CARP-0088
FILE REFERENCE: CARP-0088
CURRENT APPLICATION NUMBER: US/09/855,271
CURRENT APPLICATION NUMBER: 09/347,061
PRIOR ALILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.0%; Score 414.5; DB 10; Length 128; 65.6%; Pred. No. 1.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
61.2%; Score 416; DB 10; Length 234;
Best Local Similarity 63.5%; Pred. No. 2e-27;
Matches 80; Conservative 16; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: No. US20020042089Alel Sequence US-09-855-271-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 65.6%; pred. No. 1.5e-
Matches 80; Conservative 16; Mismatches
                                                                                           FILE REFERENCE: 037003-0275559
CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
FRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
FRIOR FILING DATE: 1999-06-18
FRIOR PILING DATE: 1995-06-07
SOFTWARE: PATCH NOS: 27
SOFTWARE: PATCH NOS: 27
SOFTWARE: PATCH NOS: 27
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Patent No. US20020042089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
              APPLICANT: MORROW, PHILLIP
                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-740-002-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TKLEIK 126
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LENGTH: 128
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                                                                                                                                                                                     AFFLICANT. CONT. Renneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.5%; Score 418.5; DB 10; Length 142; 63.0%; Pred. No. 7.8e-28; Live 17; Mismatches 29; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: April 9, 1997
ATTORNEY/AGENT INFORMATION:
NAME: POLIZZI, CAtherine M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 30414-20004.01
TELEPOMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 494-0792
TELER: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/844,736
FILING DATE: 09-Apr-1997
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: WORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                           APPLICANT: Chatterjee, Malaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                         Sequence 4, Application US/09844736
Patent No. US20020041872A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26, Application US/09740002
Patent No. US20020010198A1
GENERAL INFORMATION:
APPLICANT: BRAMS, PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 63.09
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94304-1018
121 GTKLEIK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 GTKLEIK 126
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                                                                                    09-844-736-4
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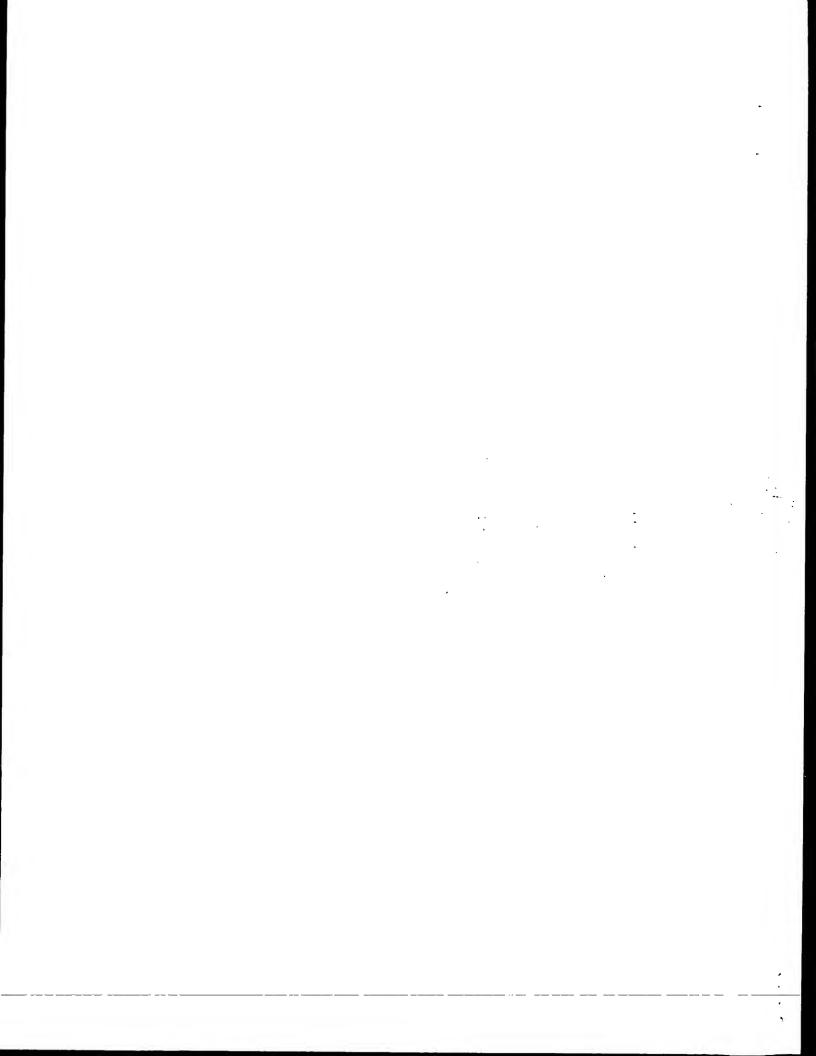
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Ор δ

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:| Db 126 VK 127

Search completed: January 6, 2003, 13:29:30 Job time: 7.10909 secs



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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 6, 2003, 13:12:26; Search time 11.7091 Seconds (without alignments) 1034.490 Million cell updates/sec Run on:

US-09-155-739-2

680 1 MRPSIQFLGLLLFWLHGAQC.....YCLQYDNLWTFGGGTKLEIK 126 Perfect score: Sequence:

Scoring table:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:* pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ain - m	ain V r	chain V r	ain V r	ain V r	chain V-J	chain - h	•	•	chain V-J	chain V-J	chain pre		chain V-J	chain - h	chain V r	chain pre	chain V r	ain pre	i.	in							
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1	ID	809365	526330	526329	C33936	S52789	S26332	PH1064	E33730	PL0270	PL0272	PL0269	PL0271	540367	540334	S40365	S40317	S40333	840352	K1HUWK	PH1063	540336	540331	842263	A29380	S52447	S24320	PL0101	952793
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	Length	125	104	104	106	129	103	97	94	107	107	107	107	127	132	139	129	125	131	129	94	124	123	117	122	127	135	128	129
æ	Query Match	86.6	78.7	77.4	77.1	ď													65.1									64.2	
	Score	. 89	m	526	~		6	488	476		465.5					•			442.5			ന	438.5	m	ζ.	ζ.	ή.	436.5	Ġ
	Result No.	-	7	m	4	'n	9	7	80	6	10	11	12	13	14	15	16	17	18	19	. 20	21	22	23	24	25	26	27	28

C;Species: Wus musculus (house mouse)
C;Date: 13-Jan-1995 #Sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26330
R;Stark, S.E.; Caton, A.J.
J. Exp. Med: 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a proteil A;Reference number: S26309; MUID:91341421; PMID:1908510

Ig kappa chain V region - mouse

A;Cross-references: EMBL:X59185; NID:952316; PIDN:CAA41895.1; PID:91334063 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin

A Status: preliminary A Molecule type: mRNA A; Residues: 1-104 <STA>

A; Accession: S26330

Ig kappa chain V r Ig kappa chain V-I	chain													
S11240 A49134	A34904	S14237	S43528	PH1224	S40316	S52792	S40350	S40349	KVMST1	S40348	S40314	803521	A23986	F36025
77	7	0	7	~	7	7	7	7	-1	7	~	a	~	7
127 2 141 2	126 2	234 2	117 2	127 2	125 2	129 2	125 2	125 2	128 1	124 2	122 2	124 2	127 2	85 2
64.0 127 2 63.9 141 2														
	63.7	63.7	63.5	63,3	63.0	62.9	62.7	62.6	62.6	62.1	61.7	61.7	61.5	61.3

ALIGNMENTS

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Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Accession: S09365
R;Feddersen, R.; van Ness, B.
Nucleic Acida Res. 17, 9797-9809, 1989
N;Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene s
A;Reference number: S09365; MUID:90098844; PMID:2513557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRPSIQFLGLLLFWLHG---DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 86.6%; Score 589; DB 2; Length 125; Best Local Similarity 90.6%; Pred. No. 5.9e-44; Matches 115; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                       A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-125 <FED>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 33-107/Domain: immunoglobulin homology <IMM>
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S26330
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Ni Alternate names: Ig kappa chain V region
C. Species: Mus musculus (house nouse)
C. Species: Mus musculus (house mouse)
C. Species: John 1908
R. Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A. Title: Antibodies that are specific for a single amino acid interchange in a proteil A. Reference number: S26309; MUD:91341421; PMID:1908510
A. Reference number: S26309; MUD:91341421; PMID:1908510
A. Residues: 1-103 <STA>
A. Molecule type: mRNA
A. Residues: Less references: EMBL:X59187; NID:952318; PIDN:CAA41897.1; PID:91334064
A. A. Recession: S26331
A. Molecule type: mRNA
A. Residues: 1-103 <ST2>
A. Res
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0
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C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Molecule type: mRNA
A Molecule type: mRNA
A Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
G;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GKRPRLLIHYTSALQPGIPSRFSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X59191; NID:g52321; PIDN:CAA41901.1; PID:g1334066 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F:16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
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ilarity 87.4%; Pred. No. 1.6e-35;
Conservative 7; Mismatches 6; Indels
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                                          81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                        DB 2;
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                                                                                                                                                                                                                                                             Ig kappa chain V region - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig light chain V region - mouse (fragment)
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Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A;Reference number: A33936; MUID:89282831; PMID:2471975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: 826329
R;Stark, S.E.; Caton, A.J.
A;Exp. Med: 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein A;Reference number: 826309; MUID:91341421; PMID:1908510
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C;Specise: Wus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C;33936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-104 CSTA>
A; Cross-references: EMBL:X59173; NID:952309; PIDN:CAA41883.1; PID:91334059
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                   Gaps
                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                     21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60
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                                                                     Length 104;
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Pred. No. 2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                3; Indels
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                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLWTFGGGTKLE 104
                                                                                                                                                                                                                                                                                                              81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLE 124
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Pred. No. 2.2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 526; DB 2;
Pred. No. 1.3e-38;
                                                                                                                      2; Mismatches
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F;16-90/Domain: immunoglobulin homology <IMM>
                                                              ch 78.7%;
1 Similarity 95.2%;
99; Conservative
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94.28;
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91.58;
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                                                                                            Local Similarity
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-106 <MEE>
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C; Species: Mus musculus (house mouse)
C; Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C; Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C; Accession: Pul0272
R; Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
J. Exp. Med. 171, 265-297, 1990
J. Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A; Reference number: PL0231; MUID: 90111618; PMID: 2104919
                                                                          C;Accession: PLO270
C;Accession: PLO270
C;Accession: PLO270
C;Accession: PLO270
T; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PLO231; MUID:90111618; PMID:2104919
A;Accession: PLO270
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                               C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
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A; Residues: 1-107 CSHL>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroteramer; immunoglobulin
F;1-23/Region: framework 1
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Best Local Similarity 85.0%; Pred. No. 2.2e-33;
Matches 91; Conservative 5; Mismatches 10; Indels
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Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)
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86.0%; Pred. No. 6.7e-34;
tive 5; Mismatches 9
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F;57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
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F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
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                                                                                                                                                                                                                                                                                                                                                                                      F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                F;24-34/Region: complementarity-determining 1
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F;50-56/Region: complementarity-determining
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Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A;Reference number: A33730; MUID:89367325; PMID:2505260
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R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both TgM and IgG anti-DNA antibodies are the products of clonally selective A;Accession: PH1064
A;Accession: PH1064
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C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                             Ig light chain V region (clone 202.54) - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
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     1 DIQMTQSPSSLSASLGGKVTFTCKASHDIKRYIAWYQHKPGKGPRLIMDYTSSLQPGIPS 60
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
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                                                         3;
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93.8%; Pred. No. 2.3e-35;
tive 3; Mismatches 3
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Best Local Similarity 93.8%
Matches 91; Conservative
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A; Residues: 1-94 <LAW>
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RESULT 11

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C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                        C; Accession: $40367
R; Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A; Title: Expressed human immunoglobulin chi genes and their hypermutation. A; Reference number: $40312; MUID:94080891; PMID:8258341
A; Accession: $40367
A; Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 LLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACCESSION: S40334
R;Klein, R.; Jaentchen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 QLGLLLLWLRGARCDIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQRKPGKAPK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 127;
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                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;33-107/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-132 <KLE>
A;Residues: 1-132 <KLE>
A;Cross-references: EMBL:X72444
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 66.7%; Score 453.5; DB 2; Best Local Similarity 68.9%; Pred. No. 2.8e-32; Matches 84; Conservative 16; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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Pred. No. 1.4e-31;
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64.6%; Pred. No. 1...
''ve 21; Mismatches
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                                         Ig kappa chain V-J-C region - human
                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: X72477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82; Conservative
                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-127 <KLE>
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                                                                    C; Accession: PL0269
R; Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.; Exp. Med. 171, 265-297, 1990
A; Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A; Reference number: PL0231; MUID:90111618; PMID:2104919
A; Accession: PL0269
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A; Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A; Reference number: PL0231; MUID:90111618; PMID:2104919
A; Accession: PL0271
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Ig kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V region (anti-DNA, 2E3VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PLO271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASLGDKVIIACRTSQDIRKNWAWYQHKAGKGPRLLIWYTSTLQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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                                                                                                                                                                                                                                                                        C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroterramer; immunoglobulin F:1‡73/Region: framework 1 F:1‡73/Region: framework 1 F:1¢-90/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.3%; Score 464.5; DB 2, 85.0%; Pred. No. 2.7e-33; Live 4; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                     F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4
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F;35-49/Region: framework 2
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Best Local Similarity 85.0%
Matches 91, Conservative
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F:89-97/Region: complementari
F:98-107/Region: framework 4
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Best Local S
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ij

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Ig Kappa chain - human

G: Species: Homo sapiens (man)

G: Species: Homo sapiens (man)

C: Species: Homo sapiens (man)

C: Species: Homo sapiens (man)

C: Accession: $40365

R: Rilein, R: Jachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A: Rilein, R: Jachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A: Rilein Expressed human immunoglobulin chi genes and their hypermutation.

A: Reference number: $40312; MUID: 94080891; PMID: 8258341

A: Reference number: $40312; MUID: 94080891; PMID: 8258341

A: Reference number: $40315

A: Residues: 1-139 < KLE>

A: Residues: 1-139 < KLE>

A: Cross-references: EMBL: X72475; NID: 9441418; PIDN: CAA51143.1; PID: 9441419

G: Superfamily: immunoglobulin homology

C: Superfamily: immunoglobulin homology 

C: Reywords: heterotetramer; immunoglobulin homology

C: Reywords: heterotetramer; immunoglobulin homology 

C: Reywords: heterotetramer; immunoglobulin homology 

C: Reywords: heterotetramer; immunoglobulin homology 

C: Reywords: heterotetramer; immunoglobulin homology 

AND OURTY MATCH

QUETY MATCH

GS. 44; Score 444.5; DB 2; Length 139;

Best Local Similarity 68.94; pred. No. 1.8e-31;

MATCHES 84; Conservative 14; Mismatches 23; Indels 1; Gaps 1;

MATCHES 84; Conservative 14; Mismatches 23; Indels 1; Gaps 1;

Ay 6 QFLGILLEWHLHGAQCDIQWTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKRPR 65
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Search completed: January 6, 2003, 13:18:18 Job time : 12.7091 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

January 6, 2003, 12:48:25; Search time 6.36364 Seconds (without alignments) 821.231 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-155-739-2 680 1 MRPSIQFLGLLFWLHGAQC......YCLQYDNLWTFGGGTKLEIK 126

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	1 homo		homo	2 homo	mus m	homo	homo	homo	homo	homod	homod	mus n	homo	homo	mus m	homo	homo	mus m	P01609 homo sapien	7 mus m	mus	P01646 mus musculu	_	homo	homo	уошо	homo	homo	homo	homod		5 mus m	P01603 homo sapien
SUMMARIES		Ð	KV1W_HUMAN	KV5E_MOUSE	KV1X_HUMAN	KV1J_HUMAN	KV5F_MOUSE	KV1B_HUMAN	KV10_HUMAN	KV1P_HUMAN	KV1Y_HUMAN	KV1A_HUMAN	KV1M_HUMAN	KV5G_MOUSE	KV4B_HUMAN	KV11_HUMAN	KV5J_MOUSE	KV1D_HUMAN	KV4C_HUMAN	KV50_MOUSE	KV1Q_HUMAN	KV5N_MOUSE	KV5K_MOUSE	KV5M_MOUSE	KV5L_MOUSE	KV1R_HUMAN	KV1C_HUMAN	KV1H_HUMAN	KV1N_HUMAN	KV1E_HUMAN	KV1V_HUMAN	KV1F_HUMAN	KV1S_HUMAN	KV5C_MOUSE	KV1K_HUMAN
		ength DB			129 1	117 1			108 1	108 1	108 1	108 1	108 1	130 1	133 1		•	•			•	108 1		•	108 1	108 1	108 1	•	•	•			108 1	115 1	108 1
di	Query	Match Length	64.9	62.6	60.7	59.1	58.8	58.5	58.2	57.7	7	56.0	55.8	55.7	55.7	55.6	55.5	55.4	55.1	55.1	54.9	54.9	54.6	54.3	54.2	53.9	53.3	53.0	52.9	52.6	52.6	52.3	52.1	52.0	51.8
		Score	441.5	425.5	412.5	402	400		395.5			380.5	379.5	378.5	378.5	378	377.5	377	375	374.5	373.5	373.5	371.5	369.5	368.5	366.5	362.5	360.5	359.5	357.5	357.5	355.5	354.5	353.5	352.5
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	P04949 mus musculu P04207 homo sapien									
KV1L_HUMAN	KV3H_HUMAN	KV3M_HUMAN	KV5H_MOUSE	KV1G_HUMAN	KV3P_MOUSE	KV5T_MOUSE	KV3L_HUMAN	KV31_MOUSE	KV5P_MOUSE	KV5Q_MOUSE
		Н	Н		-	П	Н	-	Н	-
108	129	129	117	108	110	108	129	131	108	108
51.5	51.0	51.0	50.4	50.2	50.1	49.9	49.7	49.6	49.3	49.3
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350.5	347	347	34	341.	m	333		337	335	335

ALIGNMENTS

Query Match 64.9%; Score 441.5; DB 1; Length 129; Best Local Similarity 66.9%; Pred. No. 2.6e-38; 1 Gaps 1; Matches 85; Conservative 15; Mismatches 26; Indels 1; Gaps 1; Qy 1 MRPSIQFEGILLEWILHGAQCDIQMTQSPSSLSASIGGKVTITCKTSQDINKYMAWQHKP 60 1	NATER TRANSPORT OF THE PRESENCE OF THE PRESENC	1 104AN VIW_HUMAN STANDARD; 04431; 04431; 3-AUG-1987 (Rel. 05, Last see 5-JUL-1999 (Rel. 05, Last see 5-JUL-1999 (Rel. 05, Last an gkappa chain V-I region Wallowoo saplens (Human). UMARYOCA: Metazoa: Chordata; ammalia; Eutheria; Primates; CEB_TARID-960; 1] EQUENCE FROM N.A. EQUENCE FROM N.A. EQUENCE FROM S.A. Inmunoglobulin genes of the verbill of the see of th
1 MRPSIQFLGILLEWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 	Ome	64.9%; Score 441.5; DB 1; Length 129; Similarity 66.9%; Pred. No. 2.6e-38; 5; Conservative 15; Mismatches 26; Indels 1; Gaps
	Qy Db	

121 GTKLELK 127

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KV1X_HUMAN
P04432;
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                                     KV1X_HUMAN
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                          RESULT 3
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           61 GKRPRLLIHYTSALQPGIPSRFSGSGSRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-81052342; PubMed-6776411;
Altenburger W., Steinmetz M., Zachau H.G.;
Functional and non-functional joining in immunoglobulin light chain genes of a mouse myeloma.';
Nature 287:603-607(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRPSIQFLGLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.6%; Score 425.5; DB 1; Length 128; 62.2%; Pred. No. 1.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY - DETERMINING - 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG KAPPA CHAIN V-V REGION T1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14385 MW; AFA5563D31BB7E05 CRC64;
                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-V region T1 precursor.
                                                                                                                      128 AA.
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                                                                                                                    PRT;
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; V00772; CAA24150.1; -. PIR; A01920; KVMST1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 62.29
Matches 79; Conservative
                                                                                                                     STANDARD;
                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 1
128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P80362; 1WTL
                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                          120 GTKLEIK 126
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| 123 GTRLEIK 129
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                                                                                                                   KV5E_MOUSE
P01637;
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NON_TER
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                                                                                                                                                                                                                                                                                                                                           Klobeck H.G., Combriato G., Zachau H.G.;
"Immunoglobulin genes of the kappa light chain type from two human
lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG KAPPA CHAIN V-I REGION DAUDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.7%; Score 412.5; DB 1; Length 129; 61.4%; Pred. No. 2.4e-35; Live 19; Mismatches 29; Indels 1
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FRAMEWORK-4.
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                                                                     13.40G-1987 (Rel. 05, Last sequence update)
15.JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Daudi precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                       MEDLINE=85014148; Pubmed=6091049;
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InterPro: IPR003596; Ig_V.
Pfam, PF00047; Ig; 1.
SMARY; SM00406, IGV; 1.
Immunoglobulin V region; Signal.
                                                  13-AUG-1987 (Rel. 05, Created)
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STANDARD;
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                                                                                                                                                              Homo sapiens (Human).
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Matches 78; Conserv
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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P01602;
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-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
            Pech M., Hochtl J., Schnell H., Zachau H.G.;
"Differences between germ-line and rearranged immunoglobulin V kappa coding sequences suggest a localized mutation mechanism.";
Nature 291:668-670(1981).
PIR; A01921; KYMSL6.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bence-Jones protein Au.";
Biophys. Struct. Mech. 1:139-146(1975).
-!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE
REGION OF THE KAPPA CHAIN REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schiechl H., Hilschmann N.; "Rule of antibody structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-77022433; PubMed-1234024;
Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
Schwager P., Steigemann W., Schramm H.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCLQYD 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.8%; Score 400; DB 1; Length 115; 65.2%; Pred. No. 4e-34; 1.1ve 15; Mismatches 24; Indels
                                                                                                                                                                                                                                                                       FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY - DETERMINING - 3
                                                                                                                                                                                                                                                     IG KAPPA CHAIN V-V REGION L6.
                                                                                                                                                                                                                                                                                                                                                                                                                             12986 MW; BA852C58F328E1C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972)
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region AU.
                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
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MEDLINE=81220975; PubMed=6264318;
                                                                                                                                                                  Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL 1 20
CHAIN 21 >115 IG P
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HSSP; B01607; 1REI.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 73; Conservative
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P01594;
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SEQUENCE
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                                                                                                                                                                                                            Bentley D.L., Rabbitts T.H.;
"Human immunoglobulin variable region genes -- DNA sequences of two V kappa genes and a pseudogene.";
Nature 288:730-733(1980).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GKRPRLLIHYTSALQPGIPSRFSGSGSRDYSFNISNLEPEDIATYYCLQYDN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 GKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG KAPPA CHAIN V-I REGION HK102.
FRAMEWORK-1.
COMPLEMENTARIIY-DETERMINIG-1.
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117 117
117 AA; 12768 MW; ADIDF3A40AF1A49B CRC64;
      21.JUL-1986 (Rel. 01, Created)
21.JUL-1986 (Rel. 01, Last sequence update)
15.JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region HK102 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-V region L6 precursor (Fragment).
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                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=81098966; Pubmed=6779204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J00245; AAA59087.1; -.
EMBL; Z00001; CAA77292.1; -.
PIR; A01882; K1H012.
HSSP; P01607; IREI.
Genew; HGNC:5741; IGKV1-5.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00356; Ig_V.
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SMART; SM00406; IGv; 1.
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                                                                                   Homo sapiens (Human).
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SEQUENCE FROM N.A.
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P01638;
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SEQUENCE
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last_annotation update)
                  FRAMEWORK - 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V-I region Roy.
                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                102
108
108 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hilschmann N.;
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P01608;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE-76039968; PubMed-118131;

Epp O. Lattman E.E., Schiffer M., Huber R., Palm W.;

Epp O. Lattman E.E., Schiffer M. Huber R., Palm W.;

The molecular structure of a dimer composed of the variable portions

of the Bence-Jones protein REI refined at 2.0-A resolution.";

Biochemistry 14:4943-4952(1975).

I. MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                         Gaps
                                                                                                                                                                                        21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Rei.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                         1;
                                                                                                                                                  ch 58.5%; Score 397.5; DB 1; Length 108; .1 Similarity 70.1%; Pred. No. 6.7e-34; 75; Conservative 14; Mismatches 17; Indels 1
                                                            FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                  COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01873; KIHURE.
PDB; IREI; 17-FEB-P
InterPro; IPRO33066; Ig_MHC.
InterPro; IPRO33066; Ig_V.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Bence-Jones protein; 3D-structure.
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COMPLEMENTARITY-DETERMINING-2,
FRAMEWORK-3,
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                                                                                                                                                                                                                              81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                                                                          E8011187EE6F6FB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
                                 protein.
                                                                                                                                                                                                                                                                                                   108 AA
                                                                                                             BY SIMILARITY
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                                          FRAMEWORK-1
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                                 Bence-Jones
                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=76023758; PubMed=809329;
                                                                                                                                11939 MW;
InterPro; IPR003596; Ig_v
           Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region;
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AA;
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P01607;
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Best Local
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1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS TO 39 AND 41.
Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;
(In) Franck P., Shugar D. (eds.);
Gamma globulins: structure and function, pp.57-74, Academic Press,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York (1969).
-1- MISCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 108;
COMPLEMENTARITY - DETERMINING-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEI 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 58.2%; Score 395.5; DB 1;
Best Local Similarity 71.7%; Pred. No. 1.1e-33;
Matches 76; Conservative 13; Mismatches 16;
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-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01874; K1HURY.
HSSP; P80362; IWTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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21 DIQMIQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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                                                                                                   1 DIQMIQSPSSLSASVGDRVTITCRASQDITNYVNWFQQRPGQAPKVLIYGASILETGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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57.3%; Score 389.5; DB 1; Length 108; 67.3%; Pred. No. 4.4e-33;
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COMPLEMENTARITY-DETERMINING-1:
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                                                                                                                                                       81 RESGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                          11992 MW; E3B3B246C18F0C4F CRC64;
                     ; Pred. No. 4.4e-33; 18; Mismatches 16
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Lay.
                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-ppa chain V-I region AG.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                          108 AA
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                                         72; Conservative
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                       Best Local Similarity
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DOMAIN
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P01605;
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P01593;
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MEDLINE-95086080; PubMed-7993911;
Huang D.-B., Chang C.-H., Alnsworth C., Bruenger A.T., Eulitz M.,
Solmon A., Stevens F.J., Schiffer M.;
"Comparison of crystal structures of two homologous proteins:
structural origin of altered domain interactions in immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M., Popp R.A., Solomon A.;
"Characterization and preliminary crystallographic data on the VL-related fragment of the human kI Bence Jones protein Wat.";
J. Mol. Biol. 147:185-193(1981).
-!-MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PDB; IWTL; 01.NOV-94.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                watch 57.7%; Score 392.5; DB 1; Length 108; Local Similarity 68.2%; Pred. No. 2.2e-33; Los 73; Conservative 18; Mismatches 15; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003596; Ig_v.
SMan; PR0047; Ig. 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Bence-Jones protein; 3D-structure.
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                                         COMPLEMENTARITY - DETERMINING - 1.
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                                                             FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                   FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                       11737 MW; D9D941B3F0FAE697 CRC64;
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TN -> SD (IN REF. 2).
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region WAT.
       protein.
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       region; Bence-Jones
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MEDLINE-81267384; Pubmed-6167731;
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InterPro; IPR003596; Ig_v.
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         .mmunoglobulin V
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P80362;
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           SHILLIFFE
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Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
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                                                                                SEQUENCE OF 23-130.
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                                                                                                                                                                           kappa chains.";
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P06313;
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SEQUENCE
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"Complete amino acid sequence of the variable domains of two human
"Complete amino acid sequence of the variable domains of two human
1gM anti-gamma globulins (Lay/Pom) with shared idiotypic
specificities.";
Scand. J. Immunol. 5:677-684(1976).
-!- MISCELIANDOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
-!- MISCELIANDOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
PIRS. A01871; KJHULY.
HSSP: P01607; IREI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
MEDLINE=79221900; PubMed=111146;
Seidman J.G., Max E.E., Leder P.;
"A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.";
Nature 280:370-375(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burstein Y., Schechter I.; "Amino acid sequence of the NH2-terminal extra piece segments of the precursors of mouse immunoglobulin lambdal-type and kappa-type light
                   Eukaryota; Metazoa; Chordata, Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
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                                                                                                                                      MEDLINE=77038198; PubMed=824717;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71; Conservative
Homo sapiens (Human).
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Matches 71; Conserv
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                                                                    NCBI_TaxID=9606;
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DISULFID
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL quistation -
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Nucleic Acids Res. 13:6515-6529(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Subgroup IV of human immunoglobulin K light chains is encoded by a
MEDLINE-67056897; PubMed=4162931;
Gray W.R., Dreyer W.J., Hood L.;
"Mechanism of antibody synthesis: size differences between mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                       Science 155:465-467(1967).
-1- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01922; KYMSM4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG KAPPA CHAIN V-V REGION MOPC 41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 55.7%; Score 378.5; DB 1; Length 130; Best Local Similarity 59.1%; Pred. No. 7.2e-32; Matches 75; Conservative 13; Mismatches 38; Indels 1.
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                                                                                                                                                                                                                                                                                                     Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
Pfam; PF000047; Ig; 1.
SMARY; SMO0406; IGY; 1.
Immunoglobulin V region; Signal; Bence-Jones protein.
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-IV region JI precursor.
Homo sapiens (Human).
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bentley D.L., Rabbitts T.H.;
"Evolution of immunoglobulin V genes: evidence indicating that
recently duplicated human V kappa sequences have diverged by gene
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                             IG KAPPA CHAIN V-IV REGION JI. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region HK101 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 55.7%; Score 378.5; DB 1; Local Similarity 57.9%; Pred. No. 7.4e-32; les 73; Conservative 20; Mismatches 26;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Fam, PF00047; ig; 1.
SMART; SM00406; IGV!
Immunoglobulin V region; Signal.
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MEDLINE-81098966; PubMed=6779204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14632 MW;
                                                                                                                                                                 EMBL; 200022; CAA77317.1; -. PIR; A01904; K4HUJI.
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TKVEIK 132
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P01601;
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SEQUENCE
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ID KV11_HI

MCV1_HI

MCV1_H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Schiff C., Fougereau M.;

Schiff C., Fougereau M.;

Schiff C., Fougereau M.;

Schiff C., Fougereau M.;

Schiff C., Fougereau M.;

Schiff C., Fougereau M.;

Independant of the primary structure of a mouse IgG2a immunoglobulin. Amino-acid sequence of the light chain.";

L. Eur. J. Biochem. 59:525-537(1975).

C. I. MISCELLANDOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

R. PIR, A01926; KVWS73.

R. PIGSP: PO1607; IREI.

R. InterPro; IPR003006; Ig_MHC.

R. InterPro; IPR003596; Ig_V.

R. Finest Profoud,7; ig; 1.

R. SMARY; SM00406; IGV; 1.

Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRPSIGELGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 MRVLAQLIGILLICFPGARCDIQMTQSPSSLSASVGDRVTITCRARQGISSWLAWYQQKP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata; Craniata; Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 117;
                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 12799 MW; D7DOFF3718CEF587 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 378; DB 1;
; Pred. No. 7.2e-32;
17; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-V region MOPC 173.
                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAMEWORK-2
                                                                                                                                                                                                                                                                                                                             FRAMEWORK-2
                                                                                                                                                                                                                                                  Immunoglobulin V region; Signal.
SIGNAL 1 22
CHAIN 23 >117 IG
                                                                                                   EMBL; K01322; AAA58930.1; -.
EMBL; K01324; AAA58932.1; -.
EMBL; V00558; CAAZ3824.1; -.
PIR; A01881; KIHU11.
PIR; A21056; A31056.
INTERPO; IPR003006; IQ_MHC.
InterPo; IPR003006; IQ_MC.
                                                                                                                                                                                                                                                                                                                                                                                                                                               55.6%;
62.8%;
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Best Local Similarity bicology
The Conservative
The Conservative
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                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                     117 ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                            InterPro; IPR
Pfam; PF00047
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P01643;
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SEQUENCE
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                                                                                                                                                                                                                                                                                    CHAIN
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	•	1; Gaps 1; PGIPS 80	: GVPS 60			
COMPLEMENTARITY-DETERMINING-2. FRAMENORK-3. COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4. BY SIMILARITY.	RC64; Length 108	Indels		81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126 : :	RFSGSGSGTDYSLTISBLZPZBIATYYCQQYSKLPRTFGGGTKLEIK 107	Search completed: January 6, 2003, 13:15:45 Job time : 6.36364 secs
56 88 97 108 88 108	55.58 67.39	ative	LGDRVT	ISNLEPE : : :	ISBLZPZ	у 6, 2
50 57 89 98 23 108	ius AA; nilarity	Conserv	: ///// TTSSLSAS	SGRDYSFN	SGTDYSLI	l: Januar 64 secs
DOMAIN DOMAIN DOMAIN DISULFID NON_TER	Sections Sim	12; 21 DIOMIC	1 DIQMTC	81 RFSGSG	61 RFSGSG	Search completed: Janua Job time: 6 36364 secs
		ž	<u>а</u>	λŏ	අ ව	Sea

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 6, 2003, 13:10:51; Search time 23.6727 Seconds (without alignments) 1096.702 Million cell updates/sec Run on:

US-09-155-739-2 680 1 MRPSIQFLGLLLFWLHGAQC......YCLQYDNLWTFGGGTKLEIK 126 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp_plant:*
sp_rodent:*
sp_rodent:*
sp_virus:*
sp_vortebrate:*
sp_vortebrate:*
sp_rotrus:*
sp_rvirus:*
sp_bacteriap:* Sptremal_21:*
1: sp_archea:*
2: sp_archea:*
3: sp_tung1:*
4: sp_tung1:*
5: sp_tung1:*
6: sp_mamma1:*
7: sp_mhc:*
8: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

	Description	Q921a6 mus musculu	Q8r062 mus musculu	Q91ws9 mus musculu	Q91wf8 mus muscalu	Q9u177 homo sapien		Q9rla5 mus musculu	Q9ul70 homo sapien	Q8vcp0 mus musculu	Q9j184 mus musculu	Q925s9 mus musculu	Q9ul81 homo sapien	Q920e6 mus musculu	Q9u179 homo sapien	Q9qyf0 mus musculu	Q96pf6 homo sapien
	ID	Q921A6	Q8R062	Q91WS9	Q91WF8	Q9UL77	Q96SA9	09R1A5	Q9UL70	Q8VCP0	Q9JL84	092589	Q9UL81	Q920E6	09UL79	O9OYF0	Q96PF6
	DB	11	11	11	11	4	4	11	4	11	11	11	4	11	4	11	4
	wery fatch Length DB	241	234	233	234	108	107	214	108	234	107	127	107	109	108	298	116
æ	Query	68.8	62.4	60.7	60.4	57.3	56.9	26.0	55.7	55.1	54.8	54.0	53.2	52.1	51.0	50.2	48.9
	Score	468	424.5	412.5	410.5	389.5	387	380.5	378.5	374.5	372.5	367.5	362	354.5	346.5	341.5	332.5
	Result No.	7	7	m	7	S	9	7	œ	σ	10	11	12	13	14	15	16

Q8r028 mus musculu Q920e9 mus musculu Q9u178 homo saplen Q8tcd0 homo saplen Q99m37 mus musculu	OBVIGO MUS MUSCULU OBVIJO MUS MUSCULU OBVIJO POMO SADJEN OBVIJO MUSCULU	Ugulla homo Sapien Qgulla homo sapien Qgull schistosoma Qgerzg mus musculu QRVC5f mus musculu		homo 2 mus oryct homo homo	Q8wuk4 homo sapien Q8wuk3 homo sapien Q9nsd6 homo sapien Q8wtu6 homo sapien Q9u182 homo sapien
Q8R028 Q920E9 Q9UL78 Q8TCD0 Q99M37	Q8VIJ0 Q8VIJ0 Q8VIJ0 Q8VIJ0	090L86 090L83 090410 09ER29	09JL78 09JL76 09JL80 09JL74 09JW12	Q9UL80 Q9JL82 Q9NOW5 Q8TBC9 Q8TE63	Q8WUK4 Q8WUK3 Q9NSD6 Q8WTU6 Q9UL82
111	11.4.1.	4 4 5 11 12	111111	4 6 4 4	ਚ ਚ ਚ ਚ ਚ
234 111 109 239 238	134 108 109 238	108	101 103 103 235	114 104 109 233 110	237 240 107 237 107
48.2 46.9 46.9	4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	444444 0.0004 4.00040	41.4 38.5 37.1 33.5	31.1 30.9 30.7 30.7 30.7
327.5 319.5 319 318 317.5	311.5 311.5 310 308.5	305.5 305.5 295.5	292.5 291.5 289.5 288.5 283	281.5 262 252.5 228 214	211.5 210 209 208.5 204.5
17 18 20 21	2222	22 28 29 30 30	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	36 37 39 40	4 4 4 4 1 4 4 4 4 2 5 4 5 5

ALIGNMENTS

RESULT 0921A6 ID 0	1 921A6 931A6	PRELIMINARY;	PRT;	241 AA.	
占	2001		Created)		
텀		(TrEMBLrel. 19,	Last sequence update)	sence u	pdate)
1 5	Anti-CFA 79 sin	single chain Fv	fragment (Fragment)	Fragm	upua ce) ent)
SO	Mus musculus (Mouse)	Mouse).			
ပ္ပ	Eukaryota; Meta	azoa; Chordata	; Crania	ta; Ver	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
200	Mammalia; Eutheri	eria; Rodentia	; Sciuro	ynathi;	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
N.	[1]				
RP	SEQUENCE FROM N.A.	N.A.			
RX	MEDLINE-98170165; Pubmed-9509426;	65; PubMed=950	9426;		
RA	Chung J.H., Chc	oi S.J., Kim H	.J., Kim	I.J.,	Choi I.H., Lee S.D.,
RA	Yi K.S., Suh P.	.G., Ryu S.H.,	Chung H	. X.	Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RI	"Cloning and ch	haracterizatio	n of CDN	As enco	·
RT	monoclonal anti	i-CEA antibody	CEN 79	cross	monoclonal anti-CEA antibody (CEA /9) cross-reactive with NCA-95 and
RT	generation of a single-chain Fv molecule (scFv).";	a single-chain	Fv mole	cule (s	cFv).";
R.	Mol. Cells 7:816-819(1997).	16-819(1997).			
DR	EMBL; U8806/; AAB48044.1;	AAB48044.1;			
DR	InterPro; IPR003006; Ig_MHC.	03006; I9_MHC.			
DR	Pfam; PF00047; 1g; 2.	19; 2.			
ЕŢ					
FT		1 241			
S	SEQUENCE 241	241 AA; 26086 MW;		87248E9	0276887248E9C771 CRC64;
õ	Query Match		Score 4	68; DE	Score 468; DB 11; Length 241;
M B	Best Local Similarity Matches 89; Conserv	Similarity 80.9%; 89; Conservative	Pred. No. 8e-44; 6; Mismatches	o. 8e-4 atches	<pre>Pred. No. 8e-44; 6; Mismatches 15; Indels 0; Gaps</pre>
οy	17 GAQCDIOMTC	OSPSSLSASLGGKV	TITCKTSO	DINKYMA	17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
ć)	SDIELECOS DESCRIPTION OF TAKENDER STATEMENT AND TAKENDER DESCRIPTION OF TAKEND			13
3	1177 00000000	goroddaugudau	ACUND TTT	JT TUNITO	
δλ	77 GIPSRFSGSC	GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK	PEDIATY	CLOYDNI	WTFGGTKLEIK 126
qq	190 GIPSRFSGSC	GIPSRESGSGSGRDYSESISNLEPEDIATYYCLHYDNLHTFGGGTKLELK	PEDIATY	CLHYDNI	HIFGGGTKLELK 239

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Mon Jan

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71 TSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.9 kba protein.
                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; 1g; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
                                                                                            234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA.
                                                                                            PRT;
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                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                      TISSUE=COTON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fetus.";
                                                                                                       Q91WF8;
                                                                                         Q91WF8
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                                                                 RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                       61 GKRPRLLIHYTSALQPGIPSRFSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                      61 DGTVKLLIYTSSLHSGVPSRFSGSGSGTHYSLTISNLEPEDIATYTCQQYSQFPFTFGS 120
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                  62.4%; Score 424.5; DB 11; Length 234; 66.1%; Pred. No. 5.2e-39; ive 11; Mismatches 31; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.7%; Score 412.5; DB 11; Length 233; 69.2%; Pred. No. 1.1e-37; Live 10; Mismatches 25; Indels 1;
                                                                                                                                                                                                                                                                                                                              31; Indels
                                                                                                                                                                                                                 Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0274118, AAH27418.1; -.
Hypothatical protein.
SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEABI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC013496; AAH13496.1; InterPro; IRR003006; Ig_MHC. Pfam; PF00047; ig; 2. Pfam; PR0017; ig; 2. PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 AA; 25781 MW; BIC184DA149A16EB CRC64;
                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.8 kba protein (Fragment).
                                                234 AA.
                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                            84; Conservative
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                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus (Mouse)
                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 GTKLEIK 126
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|121 GTKLEIK 127
                                                                                                                                                                                                         TISSUE-COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=COLON;
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                                                            Q8R062;
                                              Q8R062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q91WS9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q91WS9
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                   RESULT 2
Q8R062
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61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.4%; Score 410.5; DB 11; Length 234; Best Local Similarity 64.6%; Pred, No. 1.8e-37; Matches 82; Conservative 14; Mismatches 30; Indels 1;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015292; AMH15292.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001865; Ribosomal_S2.
Pfam; PF00047; ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 234 AA; 25929 MW; BODOBOEGEB7812D2 CRC64;
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EMBL; AF035037; AAD56273.1; -.
HSSP; P01607; IREI.
InterPro; IPR0033006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Gaps

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Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

"Cloning of CDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
ringle chain antibody (scFV)."
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF15371; AAD40242.1; ---
RESP; PO1679; ZFBJ.
RISSP; PO1679; ZFBJ.
RICEPPC; IPR003860; Ig_MRC.
RICEPPC; IPR003860; Ig_MC.
RICEPPC; IPR003860; Ig_W.
RICEPPC; IPR00386; Ig_W.
RICEPPC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                            56.0%; Score 380.5; DB 11; Length 214; 67.3%; Pred. No. 3.5e-34; Live 14; Mismatches 20; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                   214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 67.3% Matches 72; Conservative
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Kappa light chain of Mab7 (Fragment).
Was musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98375893; PubMed-9712075; Mard K.E., Cunningham M.W.; MAGDENORE.S., Shikhman A.R., Ward K.E., Cunningham M.W.; Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.; Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL; U96396; AAB68785.1;
InterPro; IPR003006; Ig_MHC.
                                                                                                                                  Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 56.9%; Score 387; DB 4; Length 107; Local Similarity 67.9%; Pred. No. 2.9e-35; nes 72; Conservative 15; Mismatches 19; Indels
                                                                                                                               Query Match 57.3%; Score 389.5; DB 4; Length Best Local Similarity 68.2%; Pred. No. 1.6e-35; Matches 73; Conservative 13; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                         61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIK 107
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                                          NON_TER 1
NON_TER 108 108
SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;
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Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
NON TER
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SEQUENCE
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09R1A5
1D 09R1A
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DT 01-M
DT 01-M
DT 01-D
DE RAPP
OS MUS 1
COC EUKRI
OC MARMIN
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                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
WH X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
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EMBL; AF035044; AAD56280.1; -.
HSSP; PO1607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR03596; Ig_V.
                                                                                                                                                108 AA
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Best Local Similarity 67.34
Matches 72; Conservative
                                                                                                                                                   PRELIMINARY;
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Mus musculus (Mouse).
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O9UL81;
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"T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 LLIHYTSALQPGIPSRFSGSGSRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                      Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC019474; ARH19474.1; InterPro; IPR003599; Ig. InterPro; IPR003599; Ig. InterPro; IPR003597; Ig_c1. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_NHC.
61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
                                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25.7 kDa protein.
                                                               234 AA
                                                                                                                                                                                                                                                                                                        Ffam; PF00047; 1g; 2.
SMART; SM00409; 1G; 2.
SMART; SM00407; IGC1; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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EMBL; AF206022; AAF69320.1; -.
                                                           PRELIMINARY;
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MEDLINE-99306687; PubMed-10380019;
MEDLINE-99306687; PubMed-10380019;
Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
From K.A., Chatterjee S.K.;
"Construction and characterization of a chimeric fusion protein
consisting of an anti-idiotype antibody mimicking a breast cancer-
associated antigen and the cytokine GM-CSF.";
Hybridoma 18:193-202(1999).
EMBL; AF124721; AAK55120.1;
-InterProf. T.PR003006; Ig_MHC.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                            Query Match 54.8%; Score 372.5; DB 11; Length 107; Best Local Similarity 68.2%; Pred. No. 1.2e-33; Matches 73; Conservative 7; Mismatches 26; Indels 1;
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HSSP; P80362; lWTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF0047; ig; l.
SMART; SM00406; IGv; l.
NON_TER 10 1 1 1 NON_TER 107 A3; 11648 MW; ACF9B1253ACA1E5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1. NON_TER 127 127 SEQUENCE 127 AA; 13794 MW; 13761BEBBB981FAS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Immunoglobulin light chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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61 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPWTFGGGTKLEIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                           Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                             Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.2%; Score 362; DB 4; Length 107; 64.2%; Pred. No. 1.7e-32; Arive 15; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Pterin-mimicking anti-idiotope kappa chain variable region
     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTDFTLTISGLQAEDFATYYCQQSYSALTFGPGTKVDIR 106
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109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 AA; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AF035033; AAD56269.1; -. HSSP; P01607; 1REL. InterPro; IPRO03006; Ig_MHC. InterPro; IPRO03006; Ig_MHC. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.
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nes 66; Conservative
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                                                                                                                                                                        NCBI_TaxID=9606;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-20183931; PubMed-10706631;
Shinohara N., Demura T., Fukuda H.;
"Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction method.";
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.0%; Score 346.5; DB 4; Length 108; ilarity 64.5%; Pred. No. 9.2e-31; Conservative 12; Mismatches 25; Indels 1.
                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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Last annotation update)
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EMBL; AB036341; BAA88633.1; -.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; APO35035; AAD56271.1; -.
HSSP; PO1607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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01-DEC-2001 (TrEMBLrel, 19, Last anno
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SMART; SM00406; IGv; 1.
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                          OM protein - protein search, using sw model
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Run on:

January 6, 2003, 12:46:55; Search time 32.5253 Seconds (without allynments) 573.557 Million cell updates/sec

US-09-155-739-4
746
I MKCSWVMFFLMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched: 908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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	23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result		Query				
No.	Score	Match	Match Length DB		ID	Description
	746	100.0		16	AAR81327	Mouse VLA-4 antibo
7	746	100.0	140	18	AAW22410	Alpha-4 integrin m
m	645	86.5		16	AAR81330	Mouse anti-VLA-4 a
4	633	84.9		17	AAW04379	Chimaeric human/mu
5	629	84.3		12	AAR11384	Variable gamma hea
ø	625	83.8		16	AAR76664	Murine ONS-21 anti
7	595			14	AAR41679	V heavy chain of r
8	593.5			18	AAW21845	Heavy chain variab
σ	591		138	19	AAW63828	Human Mab #117-10C
10	584			16	AAR81333	Human VLA-4 reshap

/note= "complementarity determining region 3" 132..140 /note= "framework region 4"

Region

Region Region

86..117 /note= "framework region 3" 118..131

Humanised alpha-4 Amino acid sequenc HNK-20 variable he Humanized VLA-4 an A heavy chain variab Humanised alpha-4 Nuclectide sequenc Heavy chain variab Heavy chain variab Heavy chain variab Anti-EGFR antibody NR- Heavy chain variab Anti-EGFR antibody NR- Heavy chain variab Anti-EGFR antibody Heavy chain variab HP1/2 Vh. Homo sa Anti-LAWA TAB HP1/2 Antibody HP1/2 heavy Anti-VLA4 Ab HP1/2 Antibody HP1/2 heavy Anti-VLA-4 antibod Murine anti-VLA-4 Heavy chain variab Sequence of the va Anti-TANK ligand m Anti-TANK ligand m MAD CT-M-01 heavy Anti-HEG MAD CTMO Murine anti-Dotuli	Murine anti-botuli VEGF antagonist an Human/murine chime Chimaeric human/mu Heavy chain variab
	2 AAY30123 2 AAB82701 5 AAR76681 7 AAW04396 2 AAR15437
142 1135 1137 1137 1137 1123 1123 1123 1120 1120 1120 1131 1130 1130	
7728 7728 7726 7726 7726 7726 7726 7736 7736 7736	0 4 w w G
505.5 506.5 112 576.5 114 576.5 115 576.5 116 539.5 117 539.5 118 524.5 119 524.5 119 524.5 119 524.5 119 524.5 119 524.5 119 524.5 521.5	5 5 501

ALIGNMENTS

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Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic; antibody engineering.
                                                                                                                                                                  50...34
55..68
/note= "framework region 2"
                                                                                                                                                                                             69..85
/note= "complementarity determining region 2"
                                                               Mouse VLA-4 antibody 21.6 light heavy variable region.
                                                                                                                                                  /note= "framework region 1"
50..54
                                                                                                                                1..19
/note= "signal peptide"
                                                                                                                       Location/Qualifiers
                AAR81327 standard; Protein; 140 AA.
                                             23-MAR-1996 (first entry)
                                                                                                       Aus musculus
                                AAR81327;
                                                                                                                        Key
Peptide
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                          The sequence represents the mouse antibody 21.6 heavy chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned colf sequences of mouse 21.6 VH and VL (see AAQ99889) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized heavy chain, amino acids H27, H28, H39, H30, H44 nd H71 in the human HC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig H chain. Plasmids encoding the chimeric antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They mainibitely be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for anti-invarve antibodies for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis;
                                                                                                                                                                                                                                                                       New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 746; DB 16; Length 140;
100.0%; Pred. No. 9.6e-60;
tive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                  Leger OJ, Saldanha J;
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                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 2; 105pp; English.
                                                                                                                                              (ATHE-) ATHENA NEUROSCIENCES INC
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                                                                        95WO-US01219.
                                                                                                            94US-0186269.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-idiotype antibodies.
                                                                                                                                                                                Bendig MM, Jones TS,
                                                                                                                                                                                                                  WPI; 1995-269276/35.
N-PSDB; AAQ99892.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 140 AA;
 WO9519790-A1
                                                                                                          25-JAN-1994;
                                                                      25-JAN-1995;
                                  27-JUL-1995
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mouse anti-alpha-4 integrin monoclonal antibody 21.6. The mouse anti-alpha-4 integrin monoclonal antibody 21.6. The mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VH can be incorporated into a human 21/28 CL framework to produce a claimed humanised 21.6 VH (see AMV22413) and a claimed humanised 21.6 antibody that is used in the manufacture of a medicament for treating a disease selected from asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour metastasis, mephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin generating idiotypic antibodies. The humanised antibodies of the invention have a half-life in the human isculation essentially equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This polypeptide comprises the heavy chain variable region (VH) of mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                        /label= CDR1
/note= "complementarity determining region 1"
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Best Local Similarity 100.0%; Score 746; DB 18; Length 140;
Best Local Similarity 100.0%; Pred. No. 9.6e-60;
Matches 140; Conservative 0; Mismatches 0; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                                                          'note= "framework region 1"
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                                                                                 Location/Qualifiers
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                                                                                                             'label= Leader
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/label= CDR2
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/label= FR1
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/label= FR2
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                                                Mus musculus.
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                            EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                     61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                            Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                  /label= FR4
/note= "mouse heavy light chain variable framework
                                                                                                                                                                                                                                                                                                                                /note= "mouse heavy chain variable complementarity
determining region 2"
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                                                                                                                                                                                                                                                                                                                                                                                            /note= "mouse heavy chain variable complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New humanised antibodies against VLA-4 - used for inhibiting
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    region 3"
                                                                                                                                                                                                                                       "mouse heavy chain variable framework
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                                                                                                                                                             Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                    determining region 3"
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                                                                                                                AAR81330 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  region 4"
                                                                                                                                                                                                                                               region 1"
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                                                                    121 YGNYGVYAMDYWGQGTSVTV 140
                                                            121 YGNYGVYAMDYWGQGTSVTV 140
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/label- CDR1
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                                                                                                                                                                                                                                                                                            /label= FR2
                                                                                                                                                                                                                                /label= FR1
                                                                                                                                             02-APR-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                67..98
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                                                                                                                                                                                     antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-269276/35.
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                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9519790-A1
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                                                                                                                               AAR81330;
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                                                                                                         AAR81330
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The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain variable region (without signal sequence). Cloned CDNA CDR sequences of mouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the REI antibody for the light chain and the 2*CL antibody for the heavy chain in the construction of a humanized artibody against VLA-4. The 5' and 3' ends of the mouse CDNAs are modified using PCR primers (See AAQ9895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LVCR framework are replaced by the amino caid present in the equivalent position of the mouse 21.6 Ig light chain. Plasmids encoding the chimeric antibodies are transfected into COS caid present in the equivalent position of the mouse 21.6 Ig light chain. Plasmids encoding the chimeric antibodies are transfected into COS caid present in an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the traatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DPKFQGKATITADISSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGNYAMDYWGQGTSVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSYT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heavy; variable region; murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fv region; low human antigenicity; diagnosis; treatment; cerebral tumour;
leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 86.5%; Score 645; DB 16; Length 123; Best Local Similarity 100.0%; Pred. No. 1.1e-50; Matches 121; Conservative 0; Mismatches 0; Indels 0
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/label= mat_peptide
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                                                                                                           Disclosure; Page 68; 105pp; English.
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/label= CDR_2
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/label= CDR_1
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/label= CDR_3
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                                          inflammatory disease.
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Peptide
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Claim 4; Page 18; 24pp; English.
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                                                                                                                                                                                                                                                               Riggs AD,
                                                                                                                                                                                                                                      (CITY ) CITY OF HOPE.
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Matches 123; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 AA;
                                                                                                                                                                                                                                                                                              N-PSDB; AAQ11098
                                                                                                                                                                                         19-JUL-1990;
                                                                                                                                                                                                                26-JUL-1989;
                                                                                                                                           WO9101990-A
                                                                                                                                                                   21-FEB-1991.
                                                                                                                                                                                                                                                             Shively JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR76664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                             Peptide
                                                              Region
                                                                                    Region
                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR76664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                The present sequence is the variable heavy region of the chimaeric human/murine monoclonal antibody (MAD) ONS-M21. The MAD was preped. by combining light and heavy variable region DNA. Crompan myeloblastoma cell MAD, with human light and heavy constant region sequences, respectively to produce chimaeric human/murine light and heavy chain DNA mols. A mols. Was preped, and used to transform a host cell. The heavy and light chain DNA mols. Was preped, and used to transform a host cell. The heavy and light chain DNA mols. Sepd. and connected with a peptide linker to light chain DNA mols. Sepd. and connected with a peptide linker to produce a single stranded fv region. The reshaped fv region has low human antigenicity, and is therefore expected to be useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reshaped anti-human myeloblastoma cell human antibody - has low human antigenicity, and is therefore useful for diagnosis and treatment of cerebral tumours, e.g. myeloblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAD T84.66; gamma heavy chain; carcinoembryonic antigen; CEA; human adenocarcinoma; mouse-human chimaeric antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                  84.9%; Score 633; DB 17; Length 136;
89.3%; Pred. No. 1.5e-49;
tive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variable gamma heavy chain of T84.66 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20..38
/label= tryptic peptide
/note= "sequenced as peptide fragment"
39..49
                                                                                                                                                                                              Example 2; Page 22; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR11384 standard; Protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 YVN-----QDYWGQGTSVTV 134
                                                                                          (CHUS ) CHUGAI PHARM CO LTD.
                                  94JP-0285057
                                                                    93JP-0291078.
                                                        94JP-0252166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 89.3
Matches 125; Conservative
                                                                                                                WPI; 1996-358509/36
                                                                                                                                                                                                                                                                                                                                                                      e.g. myeloblastoma.
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 136 AA;
                                                                                                                            N-PSDB; AAT38600
                                18-NOV-1994;
                                                        18-OCT-1994;
                                                                    19-NOV-1993;
            02-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR11384;
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
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The heavy chain variable region of murine MAD 84.66 was cloned and sequenced. It was used to produce mouse V-human C antibodies with high affinity for CEA. Chimaeric murine-human anti-CEA Abs are used to diagnose human colon adenocarcinomas.

See also AAQ10834-Q10848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pUC-M21-V(H); murine; ONS-M21 antibody; chimeric protein; medulloblastoma; brain tumour; treatment; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel anti-CEA antibody - comparable to ATCC Accession No. BH 8747, produced by recombinant DNA, used in diagnosis of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.3%; Score 629; DB 12; Length 140; ilarity 87.9%; Pred. No. 3.5e-49; Conservative 6; Mismatches 9; Indels
                                                                                                                                                                                                 /label= complementarity determining region 118..130
/label= complementarity determining region
                                                                                                                            50..54
/label- complementarity determining region
                                                                                                  /note= "sequenced as peptide fragment"
/label= tryptic peptide
____sequenced as peptide fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine ONS-21 antibody variable heavy chain.
                                               55..59
/label= tryptic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neumaier M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR76664 standard; Protein; 136 AA.
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us-09-155-739-4.rag

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61 EQGLEWIGRIDPANGNTKYDPRFQGKATITADTSFNTAYLQVNSLTSEDTAVYCASGGN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                      The gene fragment encoding the V heavy chain region is used to produce a genetically engineered antibody capable of reacting specifically with feline calcivirus (FCV). The antibody can be used to treat, prevent and diagnose FCV infection. It has a broad virus-neutralising spectrum and can be used to neutralise viruses which have acquired immunity to other neutralising antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                            Anti-feline calcivirus recombinant antibody - used to treat, prevent and diagnosis infection and is safe but effective in cats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complementarity determining region; CDR; heavy chain; treatment; variable region; murine; mouse; human; interleukin 5; IL-5; receptor; alpha chain; monoclonal antibody; hybridoma; detection; assay; diagnosis; allergic respiratory disease; chronic bronchitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.8%; Score 595; DB 14; Length 136; 82.9%; Pred. No. 3.9e-46;
Live 8; Mismatches 10; Indels
               /label- Complementary Determining Region 3.
                                                                                                                                                                                                                                     Tohya Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heavy chain variable region of KM1486 antibody.
                                                                                                                                                                                                                                     Maeda H, Mikami T, Nishiyama K,
                                                                                                                                                                                               (KAGA ) CHEMO SERO THERAPEUTIC RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= sig_peptide
20..137
/label= mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1-2; Figure 3; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW21845 standard; Protein; 137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AW-----LAYWGQGTLVTV 134
                                                                                                                          93EP-0103066.
                                                                                                                                                            92JP-0079189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 82.9°
Matches 116; Conservative
                                                                                                                                                                                                                                                                                          WPI; 1993-296521/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 AA;
                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ48001
                                                                                                                                                                                                                                                          Tokiyoshi S;
                                                                                                                          26-FEB-1993;
                                                                                                                                                            28-FEB-1992;
                                                                                       22-SEP-1993
                                                                                                                                                                                                                                       Kimachi K,
                                                   EP561194-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW21845;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW21845
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5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody, feline calcivirus; FCV; neutralise; heavy chain; virus; infection; diagnosis; treatment; prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ94485 is the plasmid pUC-M21-V(H), which encodes AAR76664 the murine antibody ONS-21 variable heavy chain. The plasmid was used in the construction of an expression vector, congg. cDNA encoding a human/murine chimeric antibody, reactive with human meduiloblastoma (a brain tumour) cells. The chimeric antibody can be used in the diagnosis and treatment of this
                                                                                                                                                                                                                                                                                                                                                                 Reconstituted antibody against human medullo:blastoma cells -contains high proportion of human antibody origin and has low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V heavy chain of recombinant anti-feline calcivirus antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.8%; Score 625; DB 16; Length 136;
88.6%; Pred. No. 7.7e-49;
Live 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
47..54
/label= Complementary Determining Region 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69..86
/label= Complementary Determining Region 2.
1..19
/label= sig_peptide
20..136
/label= mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR41679 standard; Protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page 59; 120pp; Japanese.
                                                                                                                                                                                                                                                                           Ohtomo T, Sato K, Tsuchiya M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94WO-JP01763.
                                                                                                                                                                                                      93JP-0291078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-1994 (first entry)
                                                                                                                                                                                                                                       (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                               WPI; 1995-200347/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 AA;
                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ94485
                                                                                                                                                                  19-OCT-1994;
                                                                                                                                                                                                      19-NOV-1993;
                                                                                         WO9514041-A1
                                                                                                                                                                                                                                                                                                                                                                                                         antigenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Sim
Watches 124;
                                                                                                                              26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR41679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Domain
Peptide
                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
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Interleukin-18: IL-18; human; treatment; autoimmune disease; Mab; immunosuppressant; inhibitor; receptor protein; detection; heavy chain; monoclonal antibody; Mab; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the heavy chain variable region of the murine anti-human interleukin 5 receptor alpha chain (hIL-5R alpha) monoclonal antibody (kMb) KM1486. KM1486 is produced by the hybridoma FERW BP-5651, which was prepared by immunising Balb/c mice with hIL-5R alpha, fusing spleen cells obtained from the mice with mouse myeloma P3-U1 cells and screening the resultant hybridomas. The MAD can be used to detect or assay for hIL-5R alpha and cells expressing it on their surface, especially to diagnose allergic respiratory diseases, e.g. chronic bronchitis. It can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody against alpha-chain of human interleukin 5 receptor useful for diagnosis and treatment of respiratory allergic diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Mab #117-10C heavy chain variable region protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.6%; Score 593.5; DB 18; Length 137; 82.9%; Pred. No. 5.4e-46;
                          69.85
/label= complementarity_determining_region_2
118.126
            /label= complementarity_determining_region_1
                                                                         /label= complementarity_determining_region_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Indels
                                                                                                                                                                                                                                                       Koike M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Pages 124-125; 238pp; Japanese.
                                                                                                                                                                                                                                                     Furuya A, Hanai N, Iida A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW63828 standard; Protein; 138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GGLRLRFFDYWGQGTTLTV 135
                                                                                                                                                                                                                         (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                               96WO-JP02588.
                                                                                                                                                                                           95JP-0232384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 116; Conservative
                                                                                                                                                                                                                                                                     Nakamura K, Takatsu K;
                                                                                                                                                                                                                                                                                                                                                                       e.g. chronic bronchitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treat such diseases.
                                                                                                                                                                                                                                                                                               WPI; 1997-202249/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 AA;
                                                                                                                                                                                                                                                                                                               N-PSDB; AAT73612
                                                                                                    WO9710354-A1
                                                                                                                                                               11-SEP-1996;
                                                                                                                                                                                          11-SEP-1995;
                                                                                                                                                                                                                                                       Anazawa H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW63828;
 Region
                             Region
                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
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δλ
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This sequence represents the human monoclonal antibody (Mab) #117-10C
heavy chain variable region which is used in a method involved in
neutralising IL18 or to treat autoimmune diseases or as an
immunosuppressant using anti-IL-18 antibodies which can inhibit IL-18.
Compared in missing anti-IL-18 antibodies which can inhibit IL-18.
Such antibodies can also be used to detect the IL-18 receptor protein
(labelled with an enzyme or a radioactive or fluorescent substance). The
protein is used to treat e.g. graft rejection, pernicious anaemia,
compressitio, insulin-resistant diabetes, Wegener granulomatosis,
discoid lupus erythematosis, ulcerative colitis, coladgiuntin-relating
discoid lupus erythematosis, ulcerative colitis, coladgiuntin-relating
cophthalmitis, hyperthyroidism, juvenile onset type diabetes, Sjogren
Syndrome, autoimmune hepatitis, autoimmune haemolytic anaemia, myasthenia
cold haemoglobinuria, polymyositis, periarteritis nodosa, multiple
cold haemoglobinuria, polymyositis, periarteritis, descentis, adisease, climacterium praecox, rheumatoid
cold haemustopyra, chronic thyroiditis, Hodgkin's disease,
cold haemoglobinuria, chick resultins, pollinosis,
arthritis, rheumatopyra, chronic thyroiditis, Hodgkin's disease,
cathiris, rheumatopyra, chronic thyroiditis, pollinosis,
aphicoxin-allergy and septic shock resulting from production or
cold haemoglobinuria, resulting from production or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New interleukin-18 receptor protein used to inhibit interleukin-18, to treat autoimmune disease and as immunosuppressant - and new monoclonal antibody and hybridoma used to detect interleukin -18
                                                                                                                                                                      79.2%; Score 591; DB 19; Length 138; 83.0%; Pred. No. 9.1e-46; tive 4; Mismatches 14; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kunikata T, Kurimoto M, Torigoe K, Ushio S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3.3a; Page 22; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
                                                                       Location/Qualifiers
                                                                                                         1..19
/label= signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97JP-0215490.
96JP-0356426.
97JP-0052526.
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Homo sapiens.
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                                                                                                                                                                                                                                                                                   EP850952-A1
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XX F X X R R R X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X X B X X B X B X X B X X B
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Sequence 142 AA;

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The sequence represents the human reshaped antibody 21.6 heavy chain variable region against leukocyte adhesion molecule VLA-4. Cloned Corned Corned Cornes Corned Cornes 
                                                                                                                                                                                                             Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                  Human VLA-4 reshaped antibody 21.6 light heavy variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
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132..142
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "complementarity determining region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "framework region 2"
                                                                                                                                                                                                                                                                                                                                                                       "signal peptide"
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                           AAR81333 standard; Protein; 142 AA
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118..131
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86..117
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55..68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory disease.
                                                                                                                                                                                                                                         antibody engineering.
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                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                             23-MAR-1996
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                                                                                      AAR81333;
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RESULT 10
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                                                                                               61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADISSNTAYLQLSSLTSEDTAVYFCAREGY 120
                      Gaps
                                                      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CDR3
/note= "21.6 complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "21.6 complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "21.6 complementarity determining region 2"
                                                                                                                                                                                                                                                                                           Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
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Score 584; DB 16; Length 142;
Pred. No. 4e-45;
                     17; Indels
                                                                                                                                                                                                                                                                          Humanised alpha-4 integrin antibody 21.6 VL version Ha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             10...142
/label= Mat_protein
/~orte= "VH version Ha (Claim 25)"
                      15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                          AAW22428 standard; Protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= Leader
                                                                                                                                121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                             YGNYGVYAMDYWGQGTLVTV 140
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/label= CDR2
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/label= CDR1
 78.3%;
ilarity 77.1%;
Conservative 1:
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/label= FR2
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                                                                                                                                                                                                                                                                                                                                                                         Chimeric Mus musculus;
Chimeric Homo sapiens;
Chimeric synthetic.
             Similarity
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              Local Sim
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   Query Match
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96WO-US18807

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WO200047625-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Gray GS,
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                    Protein
                                                            Region
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                                                                                                                                                                                                                                                                            This polypeptide, designated Ha, comprises the heavy chain variable region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also AAW22413). It is composed of complementarity determining regions from the VH region (see AAW2210) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human 21/28 CL framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate mouse and human DNA sequences. The nutagenesis of appropriate mouse and human ised 21.6 VL (see AAW22412) can be used humanised 21.6 VH and a humanised 21.6 VL (see AAW22412) can be used to produce a claimed humanised 21.6 artibody that is useful in the manufacture of a medicament for treating asthma, atherosolerosis, arthritis, transplant rejection, graft versus host disease, thumour metastasis, nephritis, aropic dermattis, psoriasis, myocardial arthritis, transplant rejection, graft versus host disease, thumour metastasis, nephritis, aropic dermattis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The humanised antibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of heavy chain variable region of 1F1 antibody.
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                                                                                                                                                                                  Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Owery Match 78.3%; Score 584; DB 18; Length 142; Best Local Similarity 77.1%; Pred. No. 4e-45; Matches 108; Conservative 15; Mismatches 17; Indels
                                                                                      Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB07967 standard; Protein; 135 AA.
                                                                                                                                                                                                                                               Example 6; Fig 11; 107pp; English.
                                                (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YGNYGVYAMDYWGQGTLVTV 140
        95US-0561521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-NOV-2000 (first entry)
                                                                                                                         WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 AA;
                                                                                                                                                N-PSDB; AAT74789
        21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB07967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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The present sequence represents the heavy chain variable region of the murine antibody IF1. The antibody has a binding specificity to B7 molecules. The antibody is used to construct humanized immunoglobulins, build comprise an antigen binding region of non-human origin and a portion of a human immunoglobulin. The humanized immunoglobulins are useful for treating autoimmune diseases, infectious diseases, infectious diseases, inflammatory disorders, systemic lupus erythematory bowel disease, inflammatory dermatitis, asthma, arthritis, inflammatory bowel disease, inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are also useful for treating artansplant recipient or preventing transplant recipient, and treating proliferative disease (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia, thalassemia and aplastic anaemia), inborn errors of metabolism, congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanized immunoglobulin having a binding specificity to B7-1 (derived from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules, modulates immune responses and can therefore treat e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goldman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "complementarity determining region 1"
                                                                                                                                               DB 21; Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Celniker AC, Collins M,
Rup B, Veldman GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20..135
/note= "mature protein"
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 8; Fig 6A; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR95948 standard; Protein; 137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carreno B,
O'hara D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infectious diseases
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99US-0339596.
                                                                                                                                                                                                                                                                                                                                                                     09-FEB-2000; 2000WO-US03303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 113; Conservative
                                                                                                                                 69..85
                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-524532/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knight A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vasquez M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA59696.
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produced by the hybridoma cell line HNK-20. This sequence represents produced by the hybridoma cell line HNK-20. This sequence represents the sequence for the antibody HNK-20 variable heavy chain. HNK-20 is a murine hybridoma cell line, that produces 19A specific for the F glycoprotein of respiratory syncytial virus (RSV). The DNA encoding these sequences were isolated using primers specific for the 5 untranslated region of the variable region, and for the introm downstream of the rearranged J region (see AAT30459-T30545 for primer sequences). The DNA encoding these sequences can be inserted into vectors containing heterologous (such as human) constant region genes, for the production of chimeric and isotype-switched antibodies. The antibodies are useful in the treatment and diagnosis of infection by RSV, such as pneumonia and bronchicilitis, in humans and animals. By using genomic DNA as a template, variable region genes can be isolated without producing fragments that have to be adapted for recombinant antibody expression.
                                                                                                                                                             Antibody; HNK-20; variable heavy chain; hybridoma; murine; IgA; mouse; F glycoprotein; respiratory syncytial virus; RSV; constant region gene; chimeric antibody; isotype-switched antibody; therapy; infection; human; pneumonia; bronchiolitis; animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR95946-R95948 represent sequences for variable regions of an antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Also, by using the genomic DNA, no knowledge of the DNA sequence encoding the target variable region is required. Chimeric antibodies produced from these proteins, that contain the constant region of the host being treated, are less likely to cause adverse immune reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding variable region of antibody HNK-20 - for treating respiratory syncytial virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Fig 5d; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-US15716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0348548.
                                                                                        HNK-20 variable heavy chain.
10-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berdoz J, Kraehenbuhl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-286826/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORAV-) ORAVAX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT30458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9616974-A1,
                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sednence
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                                                                                                                   5; Gaps
                                                                                               1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
76.5%; Score 570.5; DB 17; Length 137; 81.4%; Pred. No. 6.4e-44; Live 6; Mismatches 15; Indels 5;
                                                 Matches 114; Conservative
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61 EQGLEMIGWIDPENGNTVYDPKFQGKASITADTSSNTAXLQLSSLASEDTAVYXCA---Y 117

121 YGNYGVYAMDYWGQGTSVTV 140

121 V 121

RESULT 15 AAB07969

118 YGT -- SYWFPYWGQGTLVTV 135 RESULT 14 g

AAR81323

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The sequence encodes the mouse antibody 21.6 heavy chain variable region. Ha, directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VN (AAQ99899 and AAQ9992) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99995-98) and then subcloned into constant regions. In the humanized light chain, amino acids L45, L58 and L69 in the humanized light chain, amino acids L45, L58 and L69 in the humanized light chain, amino acids resent in the equivalent position of the mouse cransfected into COS cells. The humanized antibodies are transfected into COS cells. The humanized antibodies can be used for inhibiting adhesion of a leukocyte to an endothelial cell and contracting inflammatory diseases such as multiple sclerosis. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                          Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                        Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.9%; Score 544; DB 16; Length 123; 82.6%; Pred. No. 1.4e-41; Live 11; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Saldanha J;
AAR81323 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 69; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                               (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                           94US-0186269.
                                                                                                                                                                                                                                                                                                           95WO-US01219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 72.9%
Best Local Similarity 82.6%
Matches 100; Conservative
                                                                      02-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                     Jones IS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory disease.
                                                                                                                                                              antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 AA;
                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                               25-JAN-1994;
                                                                                                                                                                                                                                                                                                         25-JAN-1995;
                                                                                                                                                                                                                                   WO9519790-A1
                                                                                                                                                                                                                                                                       27-JUL-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Bendig MM,
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                                   AAR81323;
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autoimmune disease; infectious disease; inflammatory disorder; systemic lupus erythematosus; diabetes mellitus; insulitis; asthma; arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis; multiple sclerosis; transplant rejection; proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia; aplastic anaemia; myeloid dysplasia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanized immunoglobulin having a binding specificity to B7-1 (derived from ATCC CRL-12524) molecules, modulates immune responses and can therefore treat e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Celniker AC, Collins M, Goldman S;
Rup B, Veldman GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.85
/note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118..124
/note= "complementarity determining region 1"
                                                                                                                                    A heavy chain variable region of humanised 1F1 antibody.
                                                                                                                                                                                 B7 molecule; B7; humanised immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20..135 ___mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
AAB07969 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 10; Fig 7A; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carreno B,
O'hara D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-FEB-2000; 2000WO-US03303
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                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GS, Knight A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-524532/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAA59698
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                                                                                                                                                                                    Antibody 3D1;
                                                                                                                                                                                                                                                                                                                                                                                         Mus sp.
Homo sapiens.
                                                                                      14-NOV-2000
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24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-AUG-2000,
                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases,
                                        AAB07969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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Gray G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
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The present sequence represents the heavy chain variable region of the humanised murine antibody IP1. The antibody has a binding specificity to brownised murine antibody IP1. The antibody has a binding specificity to by molecules. The antibody is used to construct humanized immunoglobulins, which comprise an antigen binding region of non-human immunoglobulins are useful for treating autoimmune diseases, infectious diseases, inflammatory disorders, systemic lupus erythematosus, diabetes inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are also useful for treating a transplant recipient, and treating proliferative disease (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia, thanbasemia and aplastic anaemia), inborn errors of metabolism, congenital immunodeficiency diseases, and myelold dysplasia syndrome.

135 AA;

Sequence

EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120 7; Gaps 1 MKCSWVMFFLMAVVIGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60 Search completed: January 6, 2003, 13:15:16 Job time : 33.5253 secs 121 YGNYGVYAMDYWGQGTSVTV 140 Best Local Similarity 75.0% Matches 105; Conservative Query Match 61 121 δ В ŏλ g

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GenCore version 5.1.3
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OM protein - protein search, using sw model

January 6, 2003, 13:13:21; Search time 11.596 Seconds (without alignments) 355.228 Million cell updates/sec Run on:

US-09-155-739-4

1 MKCSWVMFFLMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140 Perfect score: 746 Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

262574 seqs, 29422922 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	% Ouerv				
Score	Match	Match Length DB	DB	QI.	Description
746	100.0	140	7	US-08-561-521-4	Sequence 4, Appli
746	100.0	140	S	PCT-US95-01219-4	4
645	86.5	123	~	US-08-561-521-9	6
645	86.5		2	PCT-US95-01219-9	ď
633	84.9	136	4	US-08-646-265A-29	Sequence 29, Appl
595	79.8	136	-	US-08-024-253-2	7,7
593.5	79.6	137	m	US-08-836-561-31	31,
584	78.3	142	7	US-08-561-521-17	17,
584	78.3	142	Ŋ	PCT-US95-01219-17	17,
562	75.3	125	7	US-08-561-521-44	44,
562	75.3	125	Ŋ	PCT-US95-01219-44	44,
554	74.3	136	4	US-08-348-548-8	Sequence 8, Appli
554	74.3	136	ß	PCT-US95-15716-8	8
544	72.9	123	7	US-08-561-521-11	11
544	72.9	123	'n	PCT-US95-01219-11	Sequence 11, Appl
528.5	70.8	120	7	US-07-934-373C-6	6, 7
28.5	70.8		m	US-08-437-642B-6	Sequence 6, Appli
528.5	70.8		4	US-08-146-206C-6	Sequence 6, Appli
528.5	70.8	120	S	PCT-US93-07832-6	Sequence 6, Appli
521.5	6.69	120	4	US-08-871-488A-15	15,
516	69.5	121	7	US-08-822-830B-2	Sequence 2, Appli
513	68.8	121	7	US-08-822-830B-13	Sequence 13, Appl
511	68.5	120	~	US-08-950-660-2	Sequence 2, Appli
511	68.5	120	S	PCT-US93-00030-2	Sequence 2, Appli
511	68.5	120	S	PCT-US93-00924-2	'n
505.5	67.8		6	US-08-603-024-2	'n
505.5	67.8	139	-	US-08-253-877C-8	8

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Gaps

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Query Match 100.0%; Score 746; DB 2; Length 140; Best Local Similarity 100.0%; Pred. No. 1.8e-68; Matches 140; Conservative 0; Mismatches 0; Indels C

/pp] i	Appli Appli Appli Appl	Appl Appl Appli	Appl Appl Appl	Appl	App1	Appl	Appl																												
	4, 7, 1, 13, 13, 13, 13, 13, 13, 13, 13, 13,	ത്മ് -	706	أمأذ	000	86,	86,																												
	Sequence Sequence Sequence Sequence		Sequence											Leukocyte		Crew	2000							•											
Õ	US-08-792-824-4 US-08-792-824-7 US-08-792-824-10 US-08-792-824-13	999	999	999	999	99	s-0	ALIGNMENTS		521				Humanized Antibodies Against Adhesion Molecule VLA-4		Khourie and	Tower, Sui					SC	#1.0, Version #1.25	/561,521		7186 2698	,001		33	2					
	0000									US/0856152	:	er J.	Jose Tarran	Humanized Adhesion		ld Tc	, ezt				isk	VSOC	lease.	us/08/561		817807511	994		30,2	ATIO	00	 4. 	qs		
139	254 254 254 254	136 118 113	118 642 666	255	139	137	137			on US/	:	y, Mary M.	nha, Jos S. Tal	V: Huma	;	Townsend at	rket Pla Jisco	lia		FORM:	loppy d	FC-DG-	otin Re.	BER: U	424	DATA:	5-JAN-1	FORMATI	MBER:	INFOR	-543-96 43-5043	FOR SEQ ID NO: 4:	ino aci	ar	protein
67.8	67.6 67.6 67.6 67.6	67.3 67.1 66.8	66.3 65.9	65.5	64.8	63.7				plicati	WATION	Bendig Leger,	Saldar Jones,	VENTION	EQUENCI	ENCE ADI	One Market	California	USA	EADABLE	YPE: F	S SYSTE	: Pate	TON NUM	CATION:	ICATION TON MIN	ATE: 2	SENT IN	TION NOI	ICATION	E: 415 415-5		140 amino	ling:	TYPE: p
505.5	504 504 504 504	05	494.5	າໝຸໝ	<i>,</i> α	,	- 1-		1	-08-561-521-4 Sequence 4, Application	RAL INFOR	APPLICANT: Bendig, Ma APPLICANT: Leger, Oli	PLICANT:	TITLE OF INVENTION:	NUMBER OF SEQUENCES:	ADDRESSEE	STREET:	STATE: 0	COUNTRY:	COMPUTER RI	MEDIUM T	OPERATING SYSTEM: PC-DOS/MS-DG	SOFTWARE: Patentin Re-	APPLICATION NUMBER:	CLASSIFICATION	PRIOR APPLICATION DATA:	FILING D	ATTORNEY/AGENT INFORMATION: NAME: Smith, William L.	REGISTRA	TELECOMMUNICATION INFORMA	TELEPHONE:	INFORMATION SEQUENCE C	••	TOPOLOGY	MOLECULE T 3-561-521-4
28	29 30 31	თ თ თ დ 4 ა	36 37	988	4 4	4.4	4 4		RESULT 1	US-08-5 ; Seque	GENE	; AP	; AP	IL	EN S					8													. •• •		; MC US-08-E
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RESULT 3
US-08-561-521-9
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                                                        Gaps
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APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 746; DB 5;
100.0%; Pred. No. 1.8e-68;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15270-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             Sequence 4, Application PC/TUS9501219 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
                                                                                                                      121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                        121 YGNYGVYAMDYWGQGTSVTV 140
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                                                                                                                                                                                                                                                        APPLICANT: Bendig, Mary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Smith, William L. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 140 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94105
                                                                                                                                                                                                               PCT-US95-01219-4
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80 DPKFQGKATITADISSNTAYLQLSSLTSEDIAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                       APPLICANT: Bendig, Mary M.
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 123;
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86.5%; Score 645; DB 2; Best Local Similarity 100.0%; Pred. No. 2.6e-58; Matches 121; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/186,269A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                          Eloppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application PC/TUS9501219 GENERAL INFORMATION:
Sequence 9, Application US/08561521 Patent No. 5840299 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Smith, William L. REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15, TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-5640
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-543-5043 INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-561-521-9
                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                 94105
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ZIP: 20007-5109
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US-08-024-253-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                    TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-08-646-265A-29
Sequence 29, Application US/08646265A
Sequence 29, Application US/08646265A
Sequence 20, Application US/08646265A
GENERAL INFORMATION:
APPLICANT: OHTOWO, Toshihiko
APPLICANT: SATO, Koh
TILLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY
TITLE OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                      ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: Dan Francisco STATE: California
                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 86.5%; Score 645; DB 5; L
Best Local Similarity 100.0%; Pred. No. 2.6e-58;
Matches 121; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 (186, 269 FILING DATE: 25-7An-1994
ATTORNEY, AGENT INFORMATION:
NAME: SMICH, WILLIAM L.
RECISTRATION NUMBER: 15270-14
TELECHONICATION INCORMATION:
TELECHONE: 415-543-9600
TELEFAX: 415-543-9600
                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
  Jones, S. Tarran
                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-9
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                   USA
                                                                                                                                                                                                                 94105
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61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: MAECHI, Kazuhiko
APPLICANT: MAECHI, Kazuhiko
APPLICANT: MAENA, Hiroaki
APPLICANT: TOHYAMA, Kiyoto
APPLICANT: TOHYA, Yukinobu
APPLICANT: MISHIYAMA, TUKinobu
APPLICANT: MISHIYAMI, Takeshi
TITLE OF INVENTION: ANTI-FELINE CALCIVIRUS RECOMBINANT
TITLE OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 84.9%; Score 633; DB 4; Length 136; Best Local Similarity 89.3%; Pred. No. 4.9e-57; Matches 125; Conservative 2; Mismatches 7; Indels
                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A FILING DATE: 09-SEP-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
STREET: 1233 20th Street, N.W., Suite 300
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 55,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/08024253 ; Patent No. 5785968
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 YVN-----QDYWGQGTSVTV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZONTRY: U.S.A.
ZIP: 20036-8218
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy discomputer: IBM "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: WEGNER, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C.
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61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCORMATION:

APPLICANT: Bendig, Mary M.

APPLICANT: Saldanha, Jose

APPLICANT: Saldanha, Jose

APPLICANT: Jones, S. Tarran

TITLE OF INVENTION: Humanized Antibodies Against Leukocyte

TITLE OF INVENTION: Adhesion Molecule VLA-4

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: One Market Plaza, Steuart Tower, Suite 2000

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.6%; Score 593.5; DB 3; Length 182.9%; Pred. No. 5.1e-53;
Live 6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
RECTSTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
TELEPHONE: 31-790-9091
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDENDENSES: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 17, Application US/08561521
; Patent No. 5840299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 -GGLRLRFFDYWGQGTTLTV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-561-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.8%; Score 595; DB 1; Length 136; 82.9%; Pred. No. 3.5e-53; tive 8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NOINE, ENGRANCIAL
APPLICANT: PURVYA, AKIKO
APPLICANT: INDA, Akihico
APPLICANT: INDA, Akihico
APPLICANT: ANAZAWA, Hideharu
APPLICANT: HANAI, No. 6018032uo
APPLICANT: TAKATSU, Kiyoshi
TITLE OF INVENTION: Receptor Against Human Interleukin-5
TITLE OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P-500-23744
TELECHONUSICATION INFORMATION:
TELEPHONE: (202) 887-0400
TELEFAX: (202) 835-0605
TELEFAX: 440706 WEGNEN
SEQUENCE CHARACTERISTICS:
                                                        APPLICATION NUMBER: US/08/024,253
FILING DATE: 19933301
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 79189/1992
FILING DATE: 28-FEB-1992
ATTORNEY AGENT INFORMATION:
NAME: CANTOR, Herbert I.
REGISTRATION NUMBER: 24,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: Pennie & Edmonds LLP
F: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
CLASSIFICATION: 424
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/08836561 Patent No. 6018032 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AW-----LAYWGQGTLVTV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KOIKE, Masamichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 136 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 82.98
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-836-561-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-024-253-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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17; Indels

Pred. No. 4.9e-52;

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61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                    Best Local Similarity 77.1%; Pred. No. 4.75
                                                                                                                                                                                                                                          121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                  121 YGNYGVYAMDYWGQGTLVTV 140
                                                                                                                                                                                                                                                                                                                                                                      US-08-561-521-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                              1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                       78.3%; Score 584; DB 2; Length 142; 77.1%; Pred. No. 4.9e-52; vative 15; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 15.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YGNYGVYAMDYWGQGTLVTV 140
                   TELEPHONE: 415-543-9600
TELEPRAX: 415-543-9043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 142 amino acids TYPE: amino acid
                                                                                                    LENGTH: 142 amino acids
                                                                                                                                                                                                                                               Best Local Similarity 77.1%
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                              ; MOLECULE TYPE: protein US-08-561-521-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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78.3%; Score 584; DB 5; Length 142;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 75.3%; Score 562; DB 2; Length 125; Local Similarity 89.4%; Pred. No. 7e-50; nes 110; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                          .B: Townsend and Townsend Khourie and Crew
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
Sequence 44, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFRX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Smith, William L. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94105
                                                                                                                                                                                                                                                               ADDRESSEE:
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RESULT 13
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  61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARGYYYYDSXVGYYAMDYWGQGTX 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYY -- GNYGVYAMDYWGQGTS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                               CT_CSS5-01219-44
Sequence 44, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendid, Mary M.
APPLICANT: Saldanha. Jose
APPLICANT: Saldanha. Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 562; DB 5; Length 125;
Pred. No. 7e-50;
2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                 E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE PATENTIAN STATES
SOFTWARE PATENTIAN DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: SMITH WILLIAM L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Overy Match 75.3%; Score 562; DB Best Local Similarity 89.4%; Pred. No. 7e-5 Matches 110; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 44: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 125 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                      138 VTV 140
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                                                                        121 VTV 123
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                                                                                                                                     RESULT 11
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61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
Patent No. 6258529
GENERAL INFORMATION:
APPLICANT: Berdoz, Jose
APPLICANT: Kraehenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US95-15716-8

Sequence 8, Application PC/TUS9515716

GENERAL INFORMATION:

APPLICANT: Rericos, Jose

APPLICANT: Kraehenbuhl, Jean Pierre

APPLICANT: Kraehenbuhl, Jean Pierre

TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC

TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNGLOBULIN GENES

NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS:
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80.7%; Pred. No. 5.1e-49;
tive 6; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                   ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Fish & Richardson
225 Franklin Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: CLATK, PAUL T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAS: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
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INPORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 136 antho acids
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Best Local Similarity 80.78
Matches 113; Conservative
                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-348-548-8
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ZIP: 02110-2804
COMPUTER READABLE FORM:
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STREET: ALL
TTY: Boston
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20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
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Sequence 11, Application PC/TUS9501219

Sequence 11, Application PC/TUS9501219

GENERAL INFORMATION:
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 72.9%; Score 544; DB 2; Length 123; Best Local Similarity 82.6%; Pred. No. 4.6e-48; Matches 100; Conservative 11; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTOCNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,23
APPLICATION NUMBER: US/08/186,269A FILING DATE: 25-JAN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                               NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-9603
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-11
                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08561521
Patent No. 584029
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.3%; Score 554; DB 5; Length 136; 80.7%; Pred. No. 5.1e-49; tive 6; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 2000
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                   APPLICATION NUMBER: US 08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY,FAGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
TELEFAN: (617) 542-5070
                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/15716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 YGT -- SYWFPYWGOGTLVTV 134
                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: ONE MALLES COLIY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein pCT-US95-15716-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              200154
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                                                                                                                                             FILING DATE:
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US-08-561-521-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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Sequence 27, Appl Sequence 78, Appl Sequence 4, Appli

US-09-748-960-4 US-10-006-773-1

Sequence 13, Appl Sequence 6, Appl Sequence 1, Appl Sequence 28, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 17, Appl

US-08-779-784-26 US-09-956-206A-47 US-09-974-052-1 US-09-974-051-1 US-09-974-051-1 US-09-974-051-1 US-09-974-051-1 US-09-971-543-1 US-09-911-543-1 US-09-355-925-8 US-09-355-925-8 US-09-355-925-8 US-09-355-925-8 US-09-355-925-8 US-09-355-925-8 US-09-355-925-8 US-09-355-925-8 US-09-355-925-8 US-09-355-925-7 US-09-355-925-7 US-09-355-925-7 US-09-355-925-7 US-09-355-925-7

Seguence 43, Seguence 2, A

ALIGNMENTS

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US-09-910-059-19
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Copyright (c) 1993 - 2003
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Maximum Match 100%
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Perfect score:
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Sequence 19, Application US/09910059

Sequence 19, Application US/09910059

Patent No. US20020142359A1

GENERAL INFORMATION:

APPLICANT: Copley, Clive G

APPLICANT: Edge, Michael Derek

APPLICANT: Emery, Stephen Charles

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod

TITLE OF INVENTION: MONBER: US/09/910,059

CURRENT PILING DATE: 1991-209

PRIOR APPLICATION NUMBER: PCT/GB97/01165

PRIOR APPLICATION NUMBER: GB 9703103.3

PRIOR PILING DATE: 1997-02-14

PRIOR FILING DATE: 1997-02-14

PRIOR PILING DATE: 1997-02-14

PRIOR PILING DATE: 1996-05-04
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
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Sequence 11, Appl
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Sequence 11, Appl
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Sequence 18, Appl
Sequence 38, Appl
Sequence 18, Appl
Sequence 7, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 28, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
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SUMMARIES

Length DB

Query Match

Result

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0.8-09-910-059-19 0.S-09-564-329A-11 0.S-09-854-811-11 0.S-09-934-773-11 0.S-09-963-620-11 0.S-09-968-953-520-11 0.S-09-968-91-38 0.S-09-968-91-38 0.S-09-910-059-11 0.S-09-910-059-11 0.S-09-910-059-11 0.S-09-910-059-11 0.S-09-976-787-29 0.S-09-965-198-28 0.S-09-865-198-28
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APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REFERENCE: 30435.540S14
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.5%; Score 488.5; DB 10; Length 136; 74.4%; Pred. No. 5.8e-32; Live 7; Mismatches 16; Indels 11;
                        FILE REFERENCE: 30435.540514
CURRENT APPLICATION NUMBER: US/09/655,153
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-10
PRIOR FILING DATE: 1997-03-10
PRIOR FILING DATE: 1997-03-10
PRIOR FILING DATE: 1997-01-12
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CURRENT FILING DATE: 2010-05-14
PRIOR PPLICATION NUMBER: 09/564,329
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
NUMBER OF SEO ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
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PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
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PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25
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SOFTWARE: Patentin Ver. 2.0
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Matches 99; Conservative
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US-09-854-811-11
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LENGIH: 136
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APPLICANT: Witte, Owen N.

APPLICANT: Witte, Owen N.

APPLICANT: Witte, Owen N.

APPLICANT: Saffan, Douglas C.

TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFERENCE: 30435.540S14

CURRENT APPLICATION NUMBER: 05/0959,326

PRIOR APPLICATION NUMBER: 06/071,141

PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 60/071,141

PRIOR FILING DATE: 1998-01-12

PRIOR PELICATION NUMBER: 60/113,230

PRIOR PELICATION NUMBER: 60/113,230

PRIOR PELICATION NUMBER: 60/113,230

PRIOR PELICATION NUMBER: 60/120,536

PRIOR PELICATION NUMBER: 60/120,536

PRIOR PELICATION NUMBER: 60/124,658

PRIOR PELICATION NUMBER: 60/124,658

PRIOR PELICATION NUMBER: 09/038,261

PRIOR PELICATION NUMBER: 09/038,261

PRIOR PELICATION NUMBER: 09/203,939

PRIOR PELICATION NUMBER: 09/203,939

PRIOR PELICATION NUMBER: 09/203,939

PRIOR PELICATION NUMBER: 09/203,939

PRIOR PELICATION NUMBER: 09/208,503

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                                                                                                                                                                                                                                Sequence 11, Application US/09564329A Patent No. US20010055751A1
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Patent No. US2002010266A1
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
                        124 YGVYAMDYWGQGTSVTV 140
                                                        121 AGYLAMDYWGQGTSVAV 137
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US-09-564-329A-11
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LENGTH: 136
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62 GWIDPENGDIEFVPKFQGKAIMTADIFSNTAYLHLSSLISEDTAVYYCKIGG----- 113
68 GRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVY 127
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Best Local Similarity 74.4%;
Matches 99; Conservative
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 AMDYWGQGTSVTV 140
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                                                                                                              128 AMDYWGQGTSVTV 140
                                                                                                                                               :||||| |||
114 ---FWGOGTLVTV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: SCID Mice US-09-963-620-11
                                                                                                                                                                                                                                                       RESULT 6
US-09-963-620-11
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APPLICANT: Walte, MODGILE E.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.540514
CURRENT APPLICATION NUMBER: US/09/934,773
CURRENT TILING DATE: 2001-08-21
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 1909-07-20
PRIOR FILING DATE: 1909-07-20
PRIOR FILING DATE: 1909-07-20
PRIOR FILING DATE: 1908-01-12
PRIOR FILING DATE: 1908-01-12
PRIOR FILING DATE: 1908-01-12
PRIOR FILING DATE: 1908-02-13
PRIOR FILING DATE: 1908-02-13
PRIOR FILING DATE: 1909-02-17
PRIOR FILING DATE: 1909-03-16
PRIOR FILING DATE: 1909-03-16
PRIOR FILING DATE: 1908-12-02
PRIOR FILING DATE: 1908-12-02
PRIOR FILING DATE: 1908-12-02
PRIOR FILING DATE: 1908-02-17
PRIOR FILING DATE: 1908-02-17
PRIOR PRIOR PRILCATION NUMBER: 09/203,939
PRIOR FILING DATE: 1909-02-17
PRIOR FILING DATE: 1908-12-02
PRIOR FILING DATE: 1908-12-02
PRIOR FILING DATE: 1908-12-02
PRIOR FILING DATE: 1908-02-17
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                                                                                                                                                                          16; Indels 11; Gaps
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                                                                                                                                                                                                                                8 FFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWI 67
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                                                                                                              Query Match 65.5%; Score 488.5; DB 10; Length 136; Best Local Similarity 74.4%; Pred. No. 5.8e-32; Matches 99; Conservative 7; Mismatches 16; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09934773
Patent No. US20020136689A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reiter, Robert E.
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AMDYWGQGTSVTV 140
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114 ---FWGQGTLVTV 123
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                          ; ORGANISM: SCID Mice US-09-854-811-11
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GENERAL INCOMMATION:
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
TILE OF INVENTION: PSCA! PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.540S14
CURRENT APPLICATION NUMBER: US/09/963,620
FRIOR PRILING DATE: 2001-09-03
PRIOR FILING DATE: 2001-09-03
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-31
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-03-16
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Pred. No. 5.8e-32;
7; Mismatches 16; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09963620 Patent No. US20020141941A1 GENERAL INFORMATION:
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APPLICATION NUMBER: PCT/FR96/01111
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REGISTRATION NUMBER: 24,025
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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ADDRESSEE:
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US-09-158-120A-18
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Publication No. US20020193561A1
GENERAL INFORMATION:
APPLICANT: CONSELLLER, EMMANUEL
BRACCO, LAURENT
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 64.8%; Score 483.5; DB 10; Length 139; Best Local Similarity 66.7%; Pred. No. 1.5e-31; Matches 94; Conservative 16; Mismatches 26; Indels 5;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APLICATION DATA:
APPLICATION NUMBER: US/09/968,851
FILING DATE: 03-OCt-2001
CLASSIFICATION: CUBROWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                GENERAL INFORMATION:
APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricia E.
ITILE OF INVENTION: Method of Inhibiting Stenosis and
ITILE OF INVENTION: Method of Inhibiting Stenosis and
ITILE OF INVENTION: Mestenosis
FILE REFERENCE: 1855.1069-003
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US 09/528,267
PRIOR PILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                            COTION: (1)...(139)
CTHER INFORMATION: YFC51.1 heavy chain variable region
NAME/KEX: SIGNAL
LOCATION: (1)...(19)
COTION: (1)...(19)
US-09-809-739-5
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DUNNER, LLP
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ZIP: 20005-3315
Patent No. US20020106369A1
                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
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7; Gaps
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Patent No. US20020102257A1
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
ITILE OF INVENTION: Human Murine Chimeric Antibodies Against
TITLE OF INVENTION: Respiratory Syncytical Virus
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 535;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 63.7%; Score 475.5; DB 9; Best Local Similarity 77.0%; Pred. No. 2.2e-30; Matches 94; Conservative 11; Mismatches 10;
                                                                                      NAME: Strauss, William L.
REGISTRATION NUMBER: 47, 214
REFERENCE/DOCKET NUMBER: 03804.0142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
INFORMATION FOR SEQ ID NO: 38:
FILING DATE: 17-JUL-1996
APPLICATION NUMBER: FR 95/08729
FILING DATE: 19-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-968-851-38
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OPERATING SYSTEM: Windows95
SOFTWARE: MS WORD 97
CURRENT APPLICATION DATA:
FILING DATE: September 21, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,592
FILING DATE: August 15, 1994
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
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Sequence 11, Application US/09910059
; Sequence 11, Application US/09910059
; Patent No. US2002014235941
; GENERAL INFORMATION:
    APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
    APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT FILING DATE: 1991-023
; PRIOR APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: EDT/CB97/01165
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR PILING DATE: 1997-05-14
; PRIOR PRILING DATE: 1996-05-04
; WUMBER OF SED ID NOS: 131
; SEQ ID NOS: 131
; SEQ ID NOS: 131
; SEQ ID NOS: 130
                                                                                                                                           APPLICANT: RUIZ, PEGTO
APPLICANT: RUIZ, PEGTO
APPLICANT: REEZ-ALON, Neta
APPLICANT: REEZ-ALON, Neta
APPLICANT: REEZ-ALON, Neta
APPLICANT: HERKEL, Johannes
TITLE OF INVENTION: IMMUNITY
FILE OF INVENTION: IMMUNITY
FILE REFERENCE: COHENA; 105/10/032,482
CURRENT APPLICATION NUMBER: US/10/032,482
CURRENT APPLICATION NUMBER: US/99/445,602
PRIOR APPLICATION NUMBER: DCT/1L98/00266
PRIOR APPLICATION NUMBER: PCT/1L98/00266
PRIOR APPLICATION NUMBER: L1 121041
PRIOR APPLICATION NUMBER: L1 121041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.5%; Score 466.5; DB 10; Length 120; 77.7%; Pred. No. 2.7e-30; Live 7; Mismatches 17; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.7%; Score 467.5; DB 9; Length 112; 78.0%; Pred. No. 2.1e-30; Live 10; Mismatches 9; Indels 7
Sequence 7, Application US/10032482 Publication No. US20020197270A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.0
                                                                                                                            Wolkowicz, Roland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92; Conservative
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                                                                                               ROTTER, Varda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mus musculus
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
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                                                                                                                                                                                                                                                     Length 117;
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; Sequence 4, Application US/09861294
; Sequence 4, Application US/09861294
; Sequence 4, Application US/09861294
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; CURRENT APPLICATION NUMBER: US/09/861, 294
; CRRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049, 540
; PRIOR FILING DATE: 1998-06-11
; PRIOR FILING DATE: 1998-06-11
                                                                                                                                                                                                                                                                                                      12; Indels
                                                                                                                                                                                                                                                   Ouery Match 63.7%; Score 475; DB 10; Best Local Similarity 76.9%; Pred. No. 5.7e-31; Matches 93; Conservative 10; Mismatches 12;
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                   INFORMATION FOR SEQ ID NO: 18:
     TELEPHONE: 973-994-1700
TELEFAX: 973-994-1744
                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 117 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                   TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-158-120A-18
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; LOCATION: (1)...(19)
US-09-861-294-4
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LENGTH: 153
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Patont No. US20020064528A1

GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TILLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT APPLICATION NUMBER: US/09/976,787
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
                                                             61.8%; Score 461; DB 10; Length 117; 76.0%; Pred. No. 7.1e-30; Live 9; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.8%; Score 461; DB 10; Length 238; 76.0%; Pred. No. 1.4e-29;
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PRIOR FILING DATE: 1999-01-29
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SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 29
LENGTH: 238
                                                                                                                          Conservative
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Best Local Similarity 76.09
Matches 92; Conservative
                              Query Match
Best Local Similarity
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US-09-865-198-22
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Patent No. US20020103345al
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methorite Reference: 11245/47102
GURRENT APPLICATION NUMBER: US/09/865,198
GURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
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               20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY
                                                 Sequence 23, Application US/09976787

Sequence 23, Application US/09976787

Sequence 23, Application US/09976787

Sequence 23, Application US/09976787

September 10, US20020064528A1

September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, September 20, S
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US-09-976-787-23
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LENGTH: 117
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 6, 2003, 13:12:26; Search time 13.0101 Seconds (without alignments)
1034.490 Million cell updates/sec Run on:

US-09-155-739-4

1 MKCSWVMFFLMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140 Perfect score: Sequence: Title:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

PIR_73:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	gamma	heavy	gamma	heavy	heavy	heavy	gamma-	ropher	heavy	heavy	heavy	heavy	heavy	single chain Fv	heavy	heavy													
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SUMMARIES	ID	S29594	S04576	S52445	PH1403	S03471	S17586	S06823	S03482	S24289	S03484	A56446	PH1012	S49220	A47271	PH1482	PH1013	PS0024	MHMS18	D37262	PL0246	A27609	JI.0076	PH1492	HVMSG7	A27646	E32513	S41374	A39276	PH1498
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	Length	178	136	137	123	120	117	122	115	116	120	268	108	221	114	140	107	139	139	66	115	139	141	135	140	107	138	249	141	140
	Query Match	80.9	80.0	76.5	76.1	72.3	70.1	6.69	0.69	67.0	9.99	66.3	66.2	99	63.3	63.1	62.6	62.5	62.3	62.0	61.9	61.9	61.7	61.5	61.5	61.3	61.3	61.1	61.1	61.0
	Score	603.5	597	570.5	567.5	539	523	521.5	515	200	498	494.5	493.5	492	472.5	471	467	466.5	464.5	462.5	461.5	461.5	460.5	459	459	457.5	457	456	455.5	455
	Result No.	7	7	٣	4	2	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Ig heavy chain pre Ig heavy chain V r	Ig heavy chain V r Ig heavy chain V r	heavy	Ig heavy chain V r Ig heavy chain V r	Ig heavy chain V r Ig heavy chain V r	Ig heavy chain V r Ig heavy chain V r	gamma	heavy	Ig heavy chain V r
PC1155 S25174	S21810 PH1484	PH1493 S37483	PH1494 PH1489	PH1486 PH1488	S41394 S20643	S38950 S40295	520646	C37262
20								~
	2 2	CV CV	CI CI	.,.,	~ ~	~ ~	(4	•
133	138 2 140 2	135 2469 2	135	140	120 2	246 2	123 2	66
				59.5 140 2 59.1 140 2				
60.9	60.9	60.6	59.9		59.0 59.0	59.0	58.8	58.7

ALIGNMENTS

	י איזייתים
• •	<pre>RESULT 1 829594 19 gamma chain (WM65) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999 C;Accession: S29594</pre>
:	A.Deymout, N. September: S29593 A.Reference number: S29593 A.Accession: S29594 A.Accession: S29594 A.Actatus: preliminary A.Rolecule type: mRNA A.Residues: 1-178 <-SER. A.Residues: 1-178 <-SER. A.Cross references: EMBL:X57857; NID:952590; FIDN:CAA40992.1; PID:952591 C.Keywords: immunoglobulin
	Query Match Best Local Similarity 88.1%; Pred. No. 2.1e-45; Matches 118; Conservative 6; Mismatches 5; Indels 5; Gaps 2;
	QY 7 MFFLMAVYJGVNSEVOLOOSGAELVKPGASYKLSCTASGFNIKDTYIHCVKORPEOGLEM 66 :
	QY 67 IGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGV 126
	Oy 127 YAMDYWGOGTSVTV 140 Db 116 YGMDYWGOGTSVTV 129
	RESULT 2 S04576 Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment) C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000 C; Accession: S04576 R; Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Eur, J. Immunol, 17, 91-95, 1987 A; Title: Molecular analysis of the murine lupus-associated anti-self response: involv A; Reference number: S04573; MUID:87133856; PMID:3102255 A; Accession: S04576 A; Molecule type: mRNA A; Residues: 1-136 < KNOF> A; Cross-references: EMBL:X14624; NID:952029; PIDN:CAA32777.1; PID:952030 C; Superfânily: immunoglobulin V region; immunoglobulin homology C; Reywords: heterotetramer; immunoglobulin F; 1-19/Domain: signal sequence #status predicted <sig>F; 20-136/Product: Ig heavy chain V region (fragment) #status predicted <mat>F; 34-117/Domain: immunoglobulin homology </mat></sig>

1;

Gaps

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Ig heavy chain V region (EB) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Mov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S1759; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A;Title: Biochemical implications from the variable gene sequences of an anti-cytochr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: O7-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S03471; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKCSWVMFFLMAVVT-GVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQR 59
                                                                                                                                                                                                                                                                     4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                              Length 123;
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A; Molocule type: protein
A; Residues: 1-43 <ROC25
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 539; DB 2; Length 120. Pred. No. 5.6e-40;
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S03471; MUID:84057768; PMID:6416834
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                                                                                                          DB 2;
                                                                                                                                  Pred. No. 1.9e-42;
3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                   76.1%; Score 567.5; 94.9%; Pred. No. 1.9
C; Keywords: heterotetramer; immunoglobulin F; 35-118/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.3%;
Matches 108; Conservative
                                                                                                                                                                 Matches 111; Conservative
                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S52445
R;Berdoz, J.; Kraehenbuhl, J.P.
R;Berdoz, J.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: PH1403
R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta
J. Exp. Med. 176, 1209-1214, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in
                                                                                                   1;
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: X82690; NID: 9673439; PIDN: CAA58011.1; PID: 9673440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 EQGLEWIGWIDPENGNTVYDPKFQCKASITADISSNTAYLQLSSIASEDTAVYYCA---Y 117
                                                                                                   Gaps
                                                                                                                                                                                          1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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                               Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;34-115/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                         12; Indels
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                        Score 597; DB 2;
Pred. No. 5.9e-45;
6; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 81.4%; Pred. No. 1.2e-42; Matches 114; Conservative 6; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 -- TYGAYAMDYWGQGTSVTV 134
                                                                                                                                                                                                                                                                                                                                                                                                                   121 YGNYGVYAMDYWGQGTSVTV 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 YGT--SYWFPYWGQGTLVTV 135
                    Query Match 80.0%;
Best Local Similarity 82.9%;
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-137 <BER>
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A; Residues: 1-123 <SHI>
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Gaps

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A; Note: this sequence was determined from the differentiated gene R: Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug J. Immunol. 129, 2554-2558, 1982
A: Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not A; Reference number: S07453; MUID: 83058021; PMID:6815271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, September 1991
A; Description: Cloning and sequencing of the cDNA coding for the variable regions of
A; Reference number: $24287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARWAGYY------FDYWGQGTTLT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross_references: EMBL:X62705; NID:951690; PIDN:CAA44584.1; PID:91333963 Cs. Superfeanily: immunoglobulin V region; immunoglobulin homology C;Keywords: immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR-EGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 VQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.0%; Score 500; DB 2; Length 11.81.0%; Pred. No. 1.3e-36; tive 9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                           Score 515; DB 2;
Pred. No. 6.6e-38;
                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig gamma chain V region (JS34/32) - mouse
                                                                                                                                                                                                                                                                                                                                                           69.0%;
83.5%;
A;Molecule type: mRNA
A;Residues: 10-115 <ROC1>
A;Cross-references: EMBL:X03219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-116 <MON>
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                                                                                                                                                                                            A; Accession: S07453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Moncharmont, B.
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S03484
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S24289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (clone IIC) - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1992 #text_change 21-Jan-2000 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000 C;Accession: 806823 R;Miller III, A.; Glasel, J.A. B. Mol. Biol. 209, 763-778, 1989 A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp A;Reference number: 806815; MUID:90064531; PMID:255519 A;Accession: 806823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBO J. 2, 867-872, 1983
A:Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, EMBO J. 2, 867-872, 1983
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C,Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C,Accession: S03482; S07453
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                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                               20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                            A;Cross-references: EMEL:X60683; NID:951820; PIDN:CAA43095.1; PID:951821
C;Superfaanly: Immunoglobulin V region; Immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: Immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
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                                                                                                                                                                 Length 117;
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                                                                                                                                                                                                                Indels
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A; Accession: S03482
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llarity 86.9%; Pred. No. 1.9e-38;
Conservative 4; Mismatches 9;
                                                                                                                                                              70.1%; Score 523; DB 2;
Similarity 85.2%; Pred. No. 1.4e-38;
14; Conservative 7; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: not compared with conceptual translation
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A; Residues: 1-122 <MIL>
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A; Molecule type: mRNA
A; Residues: 1-117 <MYL>
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Matches 104;
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Matches
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Iggamma-1 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: J9-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C;Accession: 549220
R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
submitted to the EMBL Data Library, September 1994
A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing A;Reference number: 549220
                                                                                                                                                                                                                             RTILIMAN, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A.Tillan, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A.Tillan and 196 anti-DNA antibodies are the products of clonally selective A.Faference number: PH0971; MUID:92381444; PMID:1512540
A.Accession: PH1012
A.Sactus: nucleic acid sequence not shown
A.Sactus: nucleic acid sequence not shown
A.Residues: 1-108 <TIL>
A.Residues: 1-108 <TIL>
A.Residues: 1-108 <TIL>
C.Superfimental source: B cell, strain [NZB x NZW]F1
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1012
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A; Residues: 1-221 <KIP>
A; Cross-references: EMBL: Z37502; NID: 9541778; PIDN: CAA85732.1; PID: 9541779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 APKFQDKATITADISSNTAYLQLSSLTSEDTAVYXCARRDNY----YAMDYW 108
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G; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F;1-120/Domain: V region #status predicted <VRG>
F;121-221/Domain: C region #status predicted <CRG>
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                                                                                                                         Ig heavy chain V region (clone 17p.73) - mouse (fragment)
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Best Local Similarity 79.3%; Pred. No. 1.3e-35;
Matches 96; Conservative 8; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 66.2%; Score 493.5; Local Similarity 85.8%; Pred. No. 4.6e nes 97; Conservative 3; Mismatches
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S49220
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A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se A;Reference number: S07453; MUID:83058021; PMID:6815271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Igheavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Aqcession: A56446
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J; Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on MI3 is functionally identially A;Reference number: A56446; MUID:95229583; PMID:7713873
                                                                                                                A.Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
                                               R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
EMBG J. 2, 867-872, 1983
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C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000 C;Accession: S03484; S07453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 SEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.8%; Score 498; DB 2; Length 120; 82.6%; Pred. No. 2.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 1-43 <RO22>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; 15-98/Domain: immunoglobulin homology <!MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Indels
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                                                                                                                                                                        A; Reference number: S03471; MUID:84057768; PMID:6416834
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80.3%; Pred. No. 9.5e-36;
tive 8; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
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A; R¢sidues: 1-268 <TAN>
A; R¢streferences: GB: (2001)
C; K¢ywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 10-120 <ROC1>
A; Cross-references: EMBL:X07144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity of Matches 100; Conservative
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Best Local Similarity
                                                                                                                                          hypervariable regions.
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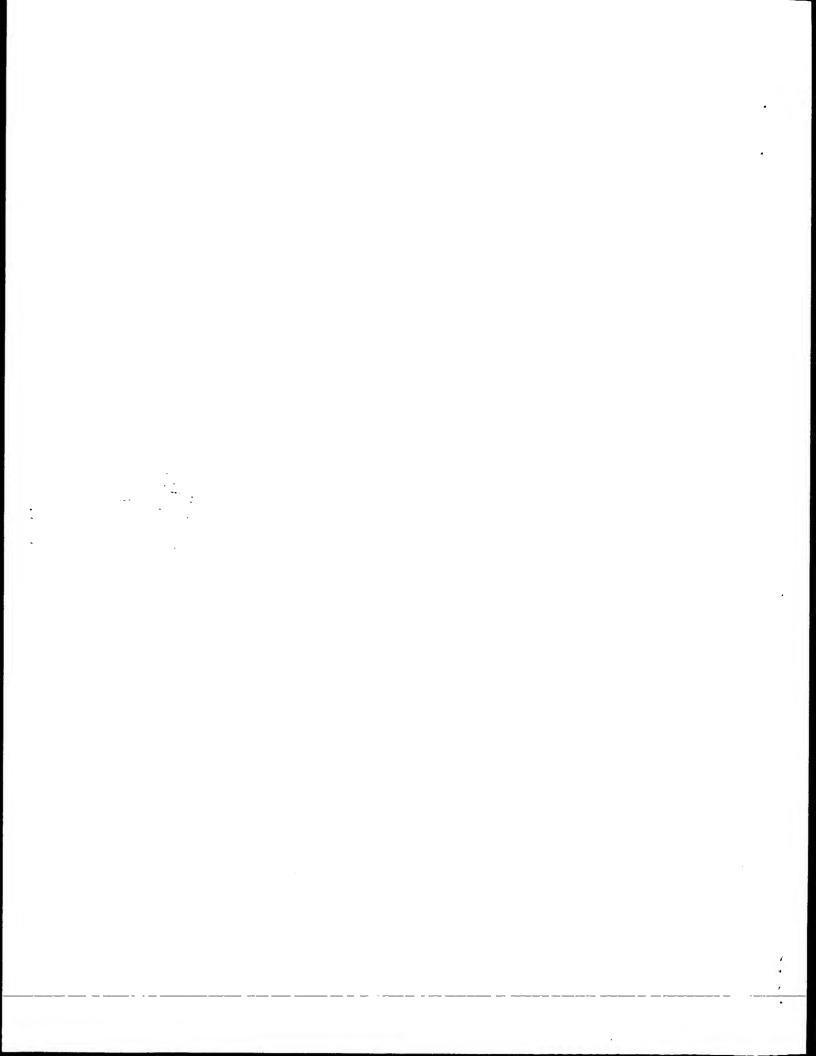
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R;Glusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that hav
                                                                                                                           RiLesley, S.A.; Parten, P.A.; Schultz, P.G. Proc. Natl. Acad. Sci. U.S.A. 90, 1160-1165, 1993
Proc. Natl. Acad. Sci. U.S.A. 90, 1160-1165, 1993
A;Title: A generic approach to the generation of antibodies with enhanced catalytic acti A;Reference number: A47271; MUID:93165660; PMID:8094556
A;Accession: A47271
nitrophenyl phosphonate-specific antibody 48G7 heavy chain VDJ - synthetic (fragment)
                                 C;Species: synthetic
A;Note: Mus musculus (house mouse) gene engineered and expressed in Escherichia coli
C;Accession: A47271
C;Accession: A47271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 DPKFQGKATITADISSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                            A.Note: sequence extracted from NCBI backbone (NCBIN:124854, NCBIP:124855)
A.Note: parts of this sequence were determined by protein sequencing
F;22-96/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DPRFQDKATITADISSKTYLQLSGLYSEDTAVYXCA--SYYG-----IYWGQGTTLT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 472.5; DB 4; Length
Pred. No. 3.2e-34;
8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: PH1482; MUID:93171820; PMID:8436910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: hybridoma cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 63.3%;
Best Local Similarity 77.7%;
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                           A; Molecule type: DNA; protein A; Residues: 1-114 <LES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-140 <GIU>
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Search completed: January 6, 2003, 13:18:19 Job time: 14.0101 secs



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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 6, 2003, 12:48:25; Search time 7.07071 Seconds (without alignments) 821.231 Million cell updates/sec Run on:

Title:
Perfect score: 7

US-09-155-739-4
746
1 MKCSWVMFFLMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		P01751 mus musculu	P01746 mus musculu	P01747 mus musculu	P01755 mus musculu	P03980 mus musculu	P01753 mus musculu	mus	P01750 mus musculu	P06328 mus musculu	mus	P01748 mus musculu	mus	P01757 mus musculu	PO1745 mus musculu	homo	P01749 mus musculu	P01756 mus musculu	P01758 mus musculu	P06330 mus musculu	P01743 homo sapien	P06329 mus musculu	P23083 homo sapien	P01783 mus musculu	P01741 mus musculu	P01808 mus musculu	P01812 mus musculu	P01742 homo sapien	P01807 mus musculu	P01805 rattus norv	P01810 mus musculu	P01809 mus musculu	P01822 mus musculu	P01795 mus musculu
SUMMENTES	ID		HV07_MOUSE	HV02_MOUSE	HV03_MOUSE	HV11_MOUSE	HV48_MOUSE	HV09_MOUSE	HV15_MOUSE	HV06_MOUSE	HV49_MOUSE	HV10_MOUSE	HV04_MOUSE	HV52_MOUSE	HV13_MOUSE	HV01_MOUSE	HV1C_HUMAN	HV05_MOUSE	HV12_MOUSE	HV14_MOUSE	HV51_MOUSE	HV1B_HUMAN	HV50_MOUSE	HV1G_HUMAN	HV16_MOUSE	HV00_MOUSE	HV38_MOUSE	HV42_MOUSE	HV1A_HUMAN	HV37_MOUSE	HV01_RAT	HV40_MOUSE	HV39_MOUSE	HV46_MOUSE	HV26_MOUSE
	DB		П	П	٦	-1	-	Н	7	Н	7	٦	-	7	-	7	П	П	-	1	٦	-	-	-	-	-	-	П	-	-	-	-	-	Н	H
	Length		139	140	120	137	138	117	136	117	117	117	117	117	117	121	147	117	117	117	118	117	120	117	136	114	119	117	117	119	142	119	118	137	144
	Query Match	:	62.3	↤	7.0	9.99	ري 8		3.1	52.7	7.7	2.1	0.7	1.1	50.8	8.0	0.7	0.1	50.1	6.6	4.6	9.5	8.3	8.1	7.8	۳. ا		2.5	'n	1.9	•	1.6	ö	39.8	8.
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	Score		464.5	459	425	422.5	416	411	396	393	393	389	388	381	379	379	378.5	374	374	372	368.5	367	360.5	359	356.5	321.5	316.5	315	314	312.5	311	310.5	304	297	297
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34 293.5 39.3 120 1 HY14_HUMAN 35 292 39.1 117 1 HY34_MOUSE 36 221.5 39.1 116 1 HY36_MOUSE 38 290 38.9 116 1 HY36_MOUSE 39 288 38.6 117 1 HY34_MOUSE 40 285.5 38.3 116 1 HY34_HUMAN 41 284.5 38.1 122 1 HY34_HUMAN 42 284 38.1 144 1 HY43_MOUSE 43 284 38.1 144 1 HY43_MOUSE 44 282.5 37.9 122 1 HY34_HUMAN 45 282 37.8 125 1 HY16_HUMAN
293.5 39.3 120 1 292 29.1 117 1 291.5 39.1 116 1 290 38.9 116 1 290 38.9 116 1 285.5 38.9 123 1 284.5 38.1 122 1 284 38.1 144 1 282.5 37.8 125 1
293.5 39.3 291.2 291.5 39.1 290.5 39.1 290.5 38.9 285.5 38.1 284.5 38.1 284.5 38.1 282.5 37.8
293.5 291.5 291.9 290 290 288.5 284.5 284.5 284.5 282.5 283.5
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ALIGNMENTS

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Query Match
                         RESULT 3
HV03_MOUSE
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                                                                              EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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                                  Gaps
                     1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
Capra J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%; Score 459; DB 1; Length 140; 63.6%; Pred. No. 2e-37; Live 18; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                        "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG HEAVY CHAIN V REGION 93G7.
  28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18; Mismatches
                                                                                                                                                                                                                                                  Ig heavy chain V region 93G7 precursor.
                                                                                                               121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                    121 YGS---SYFDYWGQGTTLTV 137
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YG--GSYDFDYWGQGTPLTV 138
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 Conservative
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                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
91;
                                                                                                                                                                                           HV02_MOUSE
P01746;
                                                                                                                                                                                                                                                                                                                                 STRAIN=A/J;
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SEQUENCE
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Matches
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antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell 24.625-637(1981).
-!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
MAKING ANTIEDDIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 VQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Heavy chain variable region contribution to the NPb family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 1g; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.0%; Score 425; DB 1;
68.3%; Pred. No. 3.1e-34;
.lve 14; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
  120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region S43 precursor.
Mus musculus (Mouse).
  PRT;
                                                                                                                 Ig heavy chain V region 36-65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEGMENT, JH2.
PIR: A02028; HYMSG7.
HSSP: P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 68.3% nes 82; Conservative
STANDARD;
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                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                        NCBI_TaxID=10090;
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P01755;
HV03_MOUSE
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                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-84248078; PubMed-6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Illegitimate recombination generates a class switch from C mu to C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.6%; Score 422.5; DB 1; Length 137; 61.4%; Pred. No. 6.3e-34; Indels 5; Albert 16; Mismatches 33; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY - DETERMINING - 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG HEAVY CHAIN V REGION S43.
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Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
PIR, A0203; HVMST7.
HSSP. 101810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-0CT-1986 (Rel. 02, Created)
23-0CT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region TEPC 1017 precursor. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAMEWORK-3.
D SEGMENT.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 LGRY----FDYWGQGTTLTV 135
                                                                                                                                                                                                                  EMBL; J00539; AAA38172.1; -. PIR; A02038; GJMS43. HSSP; P01810; 2FBJ. InterPro; IPR0033006; Ig_MHC. InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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68
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1117
1122
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SMART; SM00406; IGv; 1
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137
137 AA;
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P03980;
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SEQUENCE
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Immunoglobulin V region; Signal

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Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).

-I MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
 61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR-EG 119
 61 GGGLEWIGEINPNDGRSNYNEKFRNRATLIYDKSSSTAYMQLSSLTPEEFAVYYCARSDG 120
 Gaps
 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
 Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musicel_TaxID=10090;
 .
9
 HEAVY CHAIN V REGION TEPC 1017.
 55.8%; Score 416; DB 1; Length 138; 60.0%; Pred. No. 2.7e-33; ive 21; Mismatches 29; Indels
 Length 117;
 COMPLEMENTARITY - DETERMINING - 1.
 COMPLEMENTARITY - DETERMINING - 2.
 HEAVY CHAIN V REGION 186-1.
 COMPLEMENTARITY - DETERMINING - 1.
 COMPLEMENTARITY - DETERMINING - 2.
 COMPLEMENTARITY - DETERMINING - 3.
 147 FRAMENORK-1.
54 COMPLEMENTARITY-DETERMINING-
68 FRAMEWORK-2.
85 COMPLEMENTARITY-DETERMINING-
117 FRAMEWORK-3.
115 BY SIMILARITY.
117,
11890 MW; 16191A088CB175A CRC64;
 15576 MW; 748157E4C6907B8E CRC64;
 Score 411; DB 1;
Pred. No. 6.7e-33;
 HY09_MOUSE STANDARD; PRT; 117 AA. P01753; P11271; Created)
01-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
 BY SIMILARITY.
 IG HEAVY CH.
FRAMEWORK-1
 FRAMEWORK - 4
 FRAMEWORK - 2
 FRAMEWORK - 3
 MEDLINE=81234548; PubMed=6788376;
 Immunoglobulin V region; Signal.
 121 YYDWF-----VYWGQGTLVT 135
 PIR; B02034; HVMS61.
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGV; 1.
 120 YYGNYGVYAMDYWGQGTSVT 139
 55.1%;
68.4%;
 84; Conservative
 20
20
50
55
69
86
41
117 AA;
 138 AA;
 SEQUENCE FROM N.A.
 Best Local Similarity
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 ö
 61 EQGLEWIGRIDPANGYIKYDPKFQGKATITADISSNTAYLQLSSLTSEDTAVYFCAREGY 120
 SEQUENCE FROM N.A.
MEDLINE-82222262; PubMed-6806821;
Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
Blattner F.R.;
 Gaps
 Gaps
 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
 "Simultaneous expression of immunoglobulin mu and delta heavy chains by a cloned B-cell lymphoma: a single copy of the VH gene is shared by two adjacent CH genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
 Mús musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ;
9
 ;
 53.1%; Score 396; DB 1; Length 136; 55.7%; Pred. No. 2.2e-31;
 IG HEAVY CHAIN V REGION BCL1.
 33; Indels
 22; Indels
 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;
 21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15; Mismatches
 23; Mismatches
 Ig heavy chain V region BCL1 precursor.
 PRT;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
 121 YGNYGVYAMDYWGQGTSVTV 140
 119 YGNY----FDYWGQGTTLTV 134
 EMBL; J00494; AAA38130.1; -. PIR; A02042; HVMSB1.
 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
80; Conservative
 Conservative
 STANDARD;
 HSSP; P01772; 2FB4.
 Best Local Similarity
 NCBI_TaxID=10090;
 HV15_MOUSE
P01759;
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HV06\_MOUSE

RESULT 8

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 "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).

-- MISCELLANEOUS: THIS GERMIINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.

PIR, A070323; HWASO.

INTERPRO; IPRO03006; Ig_MHC.

InterPro; IPRO03006; Ig_W.

Pfam; PF00047; ig; 1.

SWART; SMO046; IGY; 1.
 0; Gaps
 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
 MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
 61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCA 116
 MEDLINE-85099340; PubMed-2578321;
Yancopoulos G.D., Alt F.W.;
"Dovebopmentally controlled and tissue-specific expression of unrearranged VH genee segments.";
Cell 40:271-281(1985).
 52.7%; Score 393; DB 1; Length 117; 65.5%; Pred. No. 3.6e-31;
 COMPLEMENTARITY - DETERMINING - 1.
 COMPLEMENTARITY-DETERMINING-2.
 23; Indels
 IG HEAVY CHAIN V REGION 102.
 12867 MW; 740A65DD851FCA8C CRC64;
 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region VH558 B4 precursor.
Mus musculus (Mouse).
HV06_MOUSE STANDARD; PRT; 117 AA. P01750; 21-JUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
 Query Match 52.7%; Score 393; DB J
Best Local Similarity 65.5%; Pred. No. 3.6e-:
Matches 76; Conservative 17; Mismatches
 PRT; 117 AA.
 BY SIMILARITY.
 FRAMEWORK-2.
 FRAMEWORK-1
 FRAMEWORK - 3
 Ig heavy chain V region 102 precursor.
 STANDARD;
 Mus musculus (Mouse).
 41 1
117 1
117 AA;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID=10090;
 STRAIN=C57BL/6;
 Baltimore D.;
 HV49_MOUSE
P06328;
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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 "Heavy chain variable region contribution to the NPD family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
cell 24:625-677(1981).
-!- MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
 0; Gaps
 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
 Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 61 EQGLEWIGRIDPANGYTKYDPKFQGRATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
 61 GRGLEWIGNIDPNSGGTKYNEKFKSKATLTVDKPSSTAYWQLSSLTSEDSAVYYCTR 117
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 HEAVY CHAIN V REGION VH558 B4
 Watch 52.7%; Score 393; DB 1; Length 117; Local Similarity 65.8%; Pred. No. 3.6e-31; les 77; Conservative 14; Mismatches 26; Indels
 IG HEAVY CHAIN V REGION VH558
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
 COMPLEMENTARITY-DETERMINING-2
 12834 MW; B8862FAC67ABD345 CRC64;
 MOUSE STANKE STA
 BY SIMILARITY.
 FRAMEWORK-2
 FRAMEWORK -
 PIR; A02035; MHMSB4.
HSSP; POLIBIO; ZEBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
PFam; PF00047; ig; 1.
Immunoglobulin V region; Signal.
 STRAIN=C57BL/6;
MEDLINE=81234548; PubMed=6788376;
 EMBL; J00533; AAA38602.1; -. PIR; C02034; HVMS45.
 EMBL; M13788; AAA38506.1; -.
 SEQUENCE FROM N.A.
 117 AA;
 NCBI_TaxID=10090;
 Baltimore D.;
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 Baltimore D.;
"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).
-!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
 Gaps
 Gaps
 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
 Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
 61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR 117
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
NCBI_TaxID=10090;
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 Length 117;
 COMPLEMENTARITY - DETERMINING-1.
 COMPLEMENTARITY - DETERMINING - 2
 52.1%; Score 389; DB 1; Length 117; 65.8%; Pred. No. 8.8e-31;
 COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3.
 COMPLEMENTARITY - DETERMINING - 1
 IG HEAVY CHAIN V REGION 145.
 27; Indels
 25; Indels
 IG HEAVY CHAIN V REGION 23
 12772 MW; C530F829C906F69B CRC64;
 12921 MW; D37DE8A3F543E996 CRC64;
 52.0%; Score 388; DB 1;
11arity 64.1%; Pred. No. 1.1e-30;
Conservative 15; Mismatches 27;
 Last sequence update)
Last annotation update)
 BY SIMILARITY.
 15; Mismatches
 FRAMEWORK-2.
 FRAMEWORK-2
 FRAMEWORK-3
 FRAMEWORK - 1
 FRAMEWORK-1
 HY004_MOUSE STANDARD; PRT; 1 pp.01748; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1996 (Rel. 01, Last sequence up 15-JUL-1999 (Rel. 38, Last annotation Ig heavy chain V region 23 precursor. Mus musculus (Mouse).
HSSP; P01810; ZFBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
SIGNAL
 MEDLINE=81234548; PubMed=6788376;
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 77; Conservative
 49
54
68
85
117
 49
54
 Query Match
Best Local Similarity
75; Conserve
 PIR; A02030; HVMS23
HSSP; P01810; 2FBJ.
 117 AA;
 117 AA;
 Local Similarity
 SEQUENCE FROM N.A.
 NON_TER
SEQUENCE
 NON_TER
SEQUENCE
 DISULFID
 Query Match
 CHAIN
DOMAÍN
 DOMAIN
DOMAIN
DOMAIN
DOMAIN
 DOMAIN
 SIGNAL
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 RESULT 11
HV04_MOUSE
 Matches
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140 V 140
 115 V 115
 NON_TER
SEQUENCE
 SEQUENCE.
 DISULFID
 RESULT 14
HV01_MOUSE
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
 0; Gaps
 5 WVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGL 64
 61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-Aurana (Rel. 06, Last annotation update)
17-JUL-1999 (Rel. 38, Last annotation update)
18-Mus musculus (Mouse).
19-Mus musculus (Mouse).
19-Mus musculus (Mouse).
19-Mus musculus (Mouse).
19-Musculus (
 IG HEAVY CHAIN V REGION VH558 A1/A4.
 65 EWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
 SEQUENCE FROM N.A.
MEDLINE-85099340; PubMed-2578321;
Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression of
 51.1%; Score 381; DB 1; Length 117; 65.5%; Pred. No. 5.2e-30; ive 16; Mismatches 23; Indels
 COMPLEMENTARITY-DETERMINING-1.
 COMPLEMENTARITY - DETERMINING - 2
 12971 MW; 8B0BC138856DFC9D CRC64;
 117 AA.
 BY SIMILARITY.
 FRAMEWORK - 2
 FRAMEWORK-3
 FRAMEWORK-
 PRT;
 unrearranged VH gene segments.";
 Pfam; PF00047; 19; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region; Signal.
 EMBL; M13787; AAA38499.1; -. PIR; A02029; HVMSA1.
 HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
 Conservative
 STANDARD;
 Cell 40:271-281(1985).
 117 AA;
 Local Similarity
 NCBI_TaxID=10090;
 HV52_MOUSE
P06327;
 DISULFID
NON_TER
 SEQUENCE
 Query Match
 SIGNAL
 DOMAIN
 DOMAIN
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 HV52_MOUSE
 Best Loca
Matches
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117 AA.

PRT;

STANDARD;

RESULT 13 HV13\_MOUSE ID | HV13\_MOUSE

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Zakut R., Cohen J., Givol D.;
Nucleic Acids Res. 8.4839-4640(1980).
-!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A WYELOWA THAT SECRETES IGG2B.
 80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
 6; Gaps
 20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region J558.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Schilling J., Clevinger B., Davie J.M., Hood L.;
Schilling J., Clevinger B., Davie J.M., Hood L.;
Schilling J., Clevinger B., Davie J.M., Hood L.;
Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
Nature 283:35-40(1980)
-!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALE
BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
WHICH OCCUR IN THE D AND J SEGMENTS.
-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 MEDLINE=81053741; PubMed=6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
 Length 117;
 Indels
 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
 Query Match 50.8%; Score 379; DB 1; L/Best Local Similarity 62.0%; Pred. No. 8.1e-30, Matches 75; Conservative 16; Mismatches 24;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region MPC 11.
 121 AA.
 BY SIMILARITY.
 PRT;
 PIR; A26242; MHMSJ5.
HSSP; P01789; 1MCP.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_V.
Ffan; PF00047; ig; 1.
SMART; SMO0406; IGv; 1.
Immunoglobulin V region.
 STANDARD;
 96
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID=10090;
 HV01_MOUSE
P01745;
 REVISIONS.
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Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
(In) Bach M.K. (eds.);
Immediate hypersensitivity: modern concepts and developments, pp.1-36,
 2; Gaps
 20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
 SEQUENCE FROM N.A. BEGIS656; M.Y. BOLDINES BS06524, M. BELLINES BS06524, M. Molgaard H.V., Houghton M., Derbyshire R.B., Viney J., Bell L.O., Gould H.J.; "Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line."; proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
 21-JUL-1986 (Rel. 01, Created)
LoCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 heavy chain V-I region ND precursor (Fragments).
Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
 Marcel Dekker, New York (1978).
-i- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
 Query Match 50.8%; Score 379; DB 1; Length 121; Best Local Similarity 62.0%; Pred. No. 8.4e-30; Matches 75; Conservative 17; Mismatches 27; Indels
 IG HEAVY CHAIN V-I REGION ND. PYRROLIDONE CARBOXYLIC ACID.
 SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
 T -> V (IN REF. 2).
IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
 147 AA.
 PRT;
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
 HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
PIR; A02027; GVMS11.
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
NON_TER 121 121
 STANDARD;
 PIR; A02026; E1HUND.
 SEQUENCE OF 20-147.
 NCBI_TaxID=9606;
 PROTEIN
 HV1C_HUMAN
 140 V 140
 119 V 119
 CHAIN
MOD_RES
DISULFID
 NON_TER
SEQUENCE
 CONFLICT
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16491 MW; 948F9F72A5366C20 CRC64;

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 Gaps
 9 FLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIG 68
 .;
2;
50.7%; Score 378.5; DB 1; Length 147; 52.6%; Pred. No. 1.2e-29; live 25; Mismatches 35; Indels 5,
 Search completed: January 6, 2003, 13:15:46
Job time: 8.07071 secs
 124 YGVYAMDYWGQGTSVTV 140
 Conservative
 Best Local Similarity
Matches 72; Conserv
 Query Match
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January 6, 2003, 13:10:51; search time 26:303 Seconds (without alignments) 1096.702 Million cell updates/sec
 US-09-155-739-4
746
1 MKCSWVMFFILMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140
 671580
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 671580 segs, 206047115 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 : sp_archea:*
: sp_bacteria:*
sp_fungi:*
sp_human:*
sp_human:*
sp_invertebrate:*
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 SPTREMBL_21:*
 Title:
Perfect score:
Sequence:
 Scoring table:
 Database :
 Searched:
 Run on:
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# Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

sp\_rvirus:\* sp\_bacteriap:\*

sp\_archeap:\*

sp\_vertebrate:\*

sp\_rodent:\* sp\_virus:\* sp\_plant:\*

sp\_mhc:\* sp\_organelle:\* sp\_phage:\*

SUMMARIES

| Description                   | Q99131 mus musculu                      | Q99125 mus musculu | Q9j185 mus musculu | Q9d814 mus musculu | Q8vcx7 mus musculu | Q924q3 mus musculu | Q8vcx4 mus musculu | Q8vdc9 mus musculu | Q924r4 mus musculu | Q924r1 mus musculu | Q91wt1 mus musculu | Q91wr1 mus musculu | Q924q6 mus musculu | Q991c4 mus musculu | Q91wt3 mus musculu | Q924q1 mus musculu |
|-------------------------------|-----------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| ΙD                            | Q99L31                                  | 099125             | Q9JL85             | Q9D8L4             | Q8VCX7             | 092403             | Q8VCX4             | Q8VDC9             | 0924R4             | 0924R1             | Q91WT1             | Q91WR1             | 092406             | Q99LC4             | Q91WT3             | 092401             |
| DB                            | ======================================= | 7                  | 11                 | 1                  | 11                 | 11                 | 11                 | 11                 | 1                  | 11                 | Π                  | 11                 | 11                 | 1                  | 11                 | 1                  |
| %<br>Query<br>Watch Length DB | 468                                     | 473                | 109                | 473                | 613                | 146                | 489                | 168                | 145                | 145                | 481                | 488                | 145                | 463                | 481                | 142                |
| %<br>Query<br>Match           | 79.0                                    | 66.3               | 64.3               | 64.1               | 0.09               | 59.4               | 58.8               | 58.6               | 57.8               | 57.8               | 57.5               | 57.2               | 57.0               | 57.0               | 57.0               | 56.8               |
| Score                         | 589                                     | 494.5              | 480                | 478                | 447.5              | 443                | 439                | 437                | 431.5              | 431.5              | 429                | 426.5              | 425.5              | 425.5              | 425                | 424                |
| Result<br>No.                 | -                                       | 7                  | m                  | 4                  | 2                  | 9                  | 7                  | 8                  | 6                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 |

| 092478 mus musculu 09249 mus musculu 09249 mus musculu 09247 mus musculu 09247 mus musculu 09249 mus musculu 09249 mus musculu 09249 mus musculu 09249 mus musculu 09247 mus musculu 09247 mus musculu 09480 homo sapien 09247 mus musculu 09246 mus musculu | Q9j177 mus musculu<br>Q9d9b8 mus musculu |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------|
| 0924 R B C B C B C B C B C B C B C B C B C B                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 09JL//<br>09D9BB                         |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                          |
| 04400000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 111                                      |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 51.4                                     |
| 424<br>424<br>421<br>420<br>420<br>520<br>620<br>620<br>620<br>620<br>620<br>620<br>620<br>620<br>620<br>6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 383.5                                    |
| 118<br>118<br>118<br>122<br>122<br>122<br>122<br>123<br>133<br>134<br>135<br>135<br>135<br>135<br>135<br>135<br>135<br>135<br>135<br>135                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 44<br>45                                 |
| · <u>· · · · · · · · · · · · · · · · · · </u>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                          |

## ALIGNMENTS

| RESULT<br>0991.31 | RESULT 1                                                                                           |
|-------------------|----------------------------------------------------------------------------------------------------|
| S C S             | 099131 PRELIMINARY; PRT; 468 AA.                                                                   |
| E E               | 01-JUN-2001 (TrEMBLrel, 17, Created)<br>01-JUN-2001 (TrEMBHrel, 17, Last sections indate)          |
| DT                |                                                                                                    |
| DE<br>O           | Similar to RIKEN CDNA 1810060009 gene.                                                             |
| 38                | nus muscurus (mouse).<br>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;         |
| 8                 | Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.                                 |
| Z Z               | NCBI_TaxID=10090;<br>[1]                                                                           |
| RP                | SEQUENCE FROM N.A.                                                                                 |
| RA I              | Strausberg R.;                                                                                     |
| 7 2               | Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.                                           |
| DR C              | EMBL; BCUC36/6; AAHU36/6.1;<br>HSSP: PO1842: 7FAB.                                                 |
| DR                | ٠.                                                                                                 |
| DR                | IPR003597;                                                                                         |
| Z                 | IPR003600;                                                                                         |
| DR.               | IPR003006;                                                                                         |
| 2 0               | INCEPTOS IPROGRAPS IG_V.                                                                           |
| 2 2               | FIGHT, FLOOV-1, 14, 2.                                                                             |
| DR.               | SMART; SM00407; IGC1; 3.                                                                           |
| DR                | SMART; SM00406; IGv; 1.                                                                            |
| H H               | SMART; SM00410; IG_like; 1.                                                                        |
| Z C               | PROSITE; PS00290; IG_MHC; UNKNOWN_1.<br>SECHENCE 468 AA: 51661 MW: 96352328B3332ADB CRC64:         |
| •                 |                                                                                                    |
| ŌÆ                | Query Match 79.0%; Score 589; DB 11; Length 468;<br>Best Local Similarity 81 4%; Pred No. 7 4e-50; |
| Ž                 | ative 9                                                                                            |
| δy                | 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60                                  |
| Q                 |                                                                                                    |
|                   |                                                                                                    |

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MEDLINE=20448942; PubMed=10992488;
 SEQUENCE
 NON_TER
NON_TER
 Q9D8L4
 RESULT
Q9D8L4
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61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADISSNTAYLQLSSLTSEDTAVYFCAREGY 120
 61 EQGLEWIGWIDPEDGETKYAPKFQDKATITADISSNTAYLQLSSLTSEDTAIYYCARNLL 120
 61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREG- 119
 1 MKCSWVMFFLLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
 (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 66.3%; Score 494.5; DB 11; Length 473; 67.6%; Pred. No. 1.6e-40; Live 19; Mismatches 24; Indels 3;
 Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888; AAH03888.1; -.
 Pfam; PP00047; 19; 3.
SMART; SM00409; 1G; 2.
SMART; SM00409; 1Gc1; 3.
SMART; SM00410; 1Gc1; 3.
SMART; SM00410; 1G_11ke; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 473 AA; 52449 MW; BE98B9B7986DA155 CRC64;
 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
 099L25;
091L35;
01-JUN-2001 (TrEMBLEAL. 17, Created)
01-JUN-2001 (TrEMBLEAL. 17, Last sequence update)
01-JUN-2002 (TrEMBLEAL. 21, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
 PRT;
 120 -YYGNYGVYAMDYWGQGTSVTV 140
 121 IYYG-YGLYYFDYWGQGTTITV 141
 121 YGNYGVYAMDYWGQGTSVTV 140
 121 YGGY----YDYWGQGTTITV 136
 InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003500; Ig_llke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_w.
 Conservative
 PRELIMINARY;
 PRELIMINARY;
 HSSP; P01842; 7FAB.
 Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A. STRAIN-BALB/C;
 NCBI_TaxID=10090;
 NCBI_TaxID=10090;
 96;
 Query Match
 Q9JL85;
 Q99L25
 Matches
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 RESULT 3
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CETRAINCESTBL/63; TISSUB-PANCREAS;

KRAIJUS-21085660; PubMed=11217851;

KRAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KRAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburnor M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburnor M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburnor M., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Rusha J., Marchionai L., Mashima J., Mazzarelli J., Momberts P.,

K. Marchioni L., Mashima J., Mazzarelli J., Momberts P.,

K. Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoebbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Hayashizaki Y.,

Mayashizaki Y.,

Matter Cional annotestion of a full-length mouse cDNA collection.",
 streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";
 Gaps
 28 AELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPKFQGKA 87
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 .
9
Malkiel S., Liao L., Cunningham M.W., Diamond B.; "T-Cell-dependent antibody response to the dominant epitope of
 88 TITADISSNTAYLQLSSLTSEDIAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
 Ouery Match 64.3%; Score 480; DB 11; Length 109; Best Local Similarity 80.5%; Pred. No. 7.1e-40; Matches 91; Conservative 8; Mismatches 8; Indels 6
 109 109 109 1094 MW; DFE615FE6CED4EDE CRC64;
 01-000-2001 (TrEMBLrel. 17, Created)
01-000-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
181006000981k protein.
IGH-1 OR 1810060009RIK.
 PRT; 473 AA
 Infect. Immun. 98:3803-5808(2000).
EMBL; AF206021; AAF69319.1; -
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
SMART; SM00407; ig; 1.
NON_TER
 Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1; -.
HSSP; P01842; 7FAB.
 MGD; MG196443; Igh-1.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.-11.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_like.
 PRELIMINARY;
 SEQUENCE FROM N.A.
 NCBI_TaxID-10090;
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140 V 140
 119 V 119
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092403;
 08VCX4;
 Q8VCX4
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 Q8VCX4
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 61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
 61 GHGLEWIGEILDESGSTNYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYXCAR--- 117
 Gaps
 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 67.9 kba protein.
Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
 4;
 60.0%; Score 447.5; DB 11; Length 613; 62.1%; Pred. No. 9.7e-36; Live 19; Mismatches 29; Indels 5;
 // Match 64.1%; Score 478; DB 11; Length 473; Local Similarity 67.1%; Pred. No. 6.8e-39; nes 94; Conservative 19; Mismatches 23; Indels
 Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (10EC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC018315; AAH18315.1; -.
RINTERPO: IPR003359; 1g.c1.
RINTERPO: IPR003306; 1g_MHC.
RINTERPO: IPR003306; 1g_MHC.
R Pfam; PF00047; 1g; 5.
R SMART; SM00409; IG; 2.
R SMART; SM00409; IG; 2.
R SMART; SM00406; IGV; 1.
 Hypothetical protein.
SEOUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;
 PFGMT; PF00047; 1g; 4. SMART; SM00407; 1g; 4. SMART; SM00409; 1G; 2. SMART; SM00406; 1Gv; 1. SMART; SM00410; 1G_11; 3. SMART; SM00410; 1G_11ke; 1. SMART; SM00410; 1G_11ke; 1. SMART; SM00410; 1G_MHC; UNKNOWN 1. SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
 PRT; 613 AA.
 PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 121 YGNYGVYAMDYWGQGTSVTV 140
 121 YGNYGVYAMDYWGQGTSVTV 140
 :| :| |||||| |||
121 --DYDWFA--YWGQGTLVTV 136
 118 -- RLGRWYFDVWGAGTTVTV 135
 87; Conservative
InterPro; IPR003596; Ig_v.
 PRELIMINARY;
 SEQUENCE FROM N.A.
TISSUE=SALIVARY GLAND;
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 28VCX7;
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80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
 2; Gaps
 20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
 Kozono Y., Kozono H., Azuma T.;
Rozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067797; BAB63282.1;
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
NON_TER
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Ouery Match 59.4%; Score 443; DB 11; Length 146; Best Local Similarity 71.1%; Pred. No. 4.6e-36; Matches 86; Conservative 14; Mismatches 19; Indels
 Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO18322; AAH18322.1;
MGD; MGI:2144917; AI893585.
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 53.2 kba protein.
AI893585.
 146 AA
 InterPro; IPR00359; Ig.
InterPro; IPR00359; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_wHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00409; IG; 3.
SMART; SM00400; IG; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 PRELIMINARY;
PRELIMINARY;
 [1]
SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID=10090;
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 0924R1
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 61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
 Gaps
 61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
 8; Gaps
 1 MKCSWVMFFIMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ;;
 58.8%; Score 439; DB 11; Length 489; 62.7%; Pred. No. 5.1e-35; ive 16; Mismatches 35; Indels
 58.6%; Score 437; DB 11; Length 168; 60.6%; Pred. No. 2.1e-35; ive 19; Mismatches 29; Indels
 "Targeting T cells to the CNS.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ16332; CAC94867.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig_wHC.
InterPro; IPR003596; Ig_v.
 Chernajovsky Y.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Hypothetical protein.
SEQUENCE 489 AA; 53208 MW; CC85B1194DAFEF2C CRC64;
 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;
 Last sequence update)
 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence v
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Anti-MOG 212 variable gamma 2a (Fragment).
 Pfam; PF00047; 1g; 1.
SMART; SM00409; 1G; 1.
SMART; SM00406; 1Gv; 1.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
 121 YGNY-GVYA-MDYWGQGTSVTV 140
 121 RGNYDGSLAWFVYWGQGTLVTV 142
 121 YGNYGV--YAMDYWGQGTSVTV 140
 --NYGSSRWYFDVWGAGTTVTV 136
 Odery Match
Best Local Similarity

Local Similarity

Local 86; Conservative 1
 89; Conservative
 PRELIMINARY;
 Mus musculus (Mouse).
 Ouery Match
Best Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 STRAIN-BALB/C;
 STRAIN-BALB/C;
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SEQUENCE
 Sembi P.;
 Q8VDC9;
 08VDC9
 Matches
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80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
 3; Gaps
 20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
 Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067785; BAB63270.1;
InterPro; IPR003006; Ig_MHC.
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 STRAIN-C57BL/6;

Kozono Y., Kozono H., Azuma T.;

Foliact Estimation of Relative Affinity by Flow Cytometry Reveals

"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy.3-Nitrophenyl)Acetyl (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; ABOG7789; BAB63274.1;

Enterpro; IPR00306; Ig_MHC.

Pfam; PF00047; Ig; 1.

NON_TER
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 57.8%; Score 431.5; DB 11; Length 145; 70.2%; Pred. No. 6.2e-35;
 DB 11; Length 145;
 Best Local Similarity 70.2%; Pred. No. 6.2e-35;
Matches 85; Conservative 14; Mismatches 19; Indels
 Pfam; PF00047; ig; 1.

NON_TER 1 1 1

NON_TER 145 145

SEQUENCE 145 AA; 16081 MW; ECDBIA135E05B8AA CRC64;
 145 AA; 15979 MW; 0162D0A26C746C04 CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
 Score 431.5; DB 17
Pred. No. 6.2e-35;
 145 AA.
 VH186.2-D-J-C mu protein (Fragment).
PRT;
 57.8%;
PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Query Match
Best Local Similarity
 NCBI_TaxID=10090;
 NCBI_TaxID=10090;
 STRAIN=C57BL/6;
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Gaps

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61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
 80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCARE--GYYGNYGVYAMDYWGQGTS 137
 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
 20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
 Kozono Y., Kozono H., Azuma T.;
Kozono Y., Kozono H., Azuma T.;
Albirect Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Mitrophenyl) Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
Bands12, BAB63279.1;
InterPro; IPR003006; Ig_MHC.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
 Query Match
57.2%; Score 426.5; DB 11; Length 488;
Best Local Similarity 59.6%; Pred. No. 8.6e-34;
Matches 84; Conservative 21; Mismatches 35; Indels 1;
 Match 57.0%; Score 425.5; DB 11; Length 145; Local Similarity 68.3%; Pred. No. 2.4e-34; les 84; Conservative 14; Mismatches 18; Indels 7;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC01539; ARH13391.; -. MGD; MGI:2144917; AIG93585. InterPro; IPR003006; Ig_MHC.
 Pfam; PP00047; 1g; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;
 145 AA; 16011 MW; 9BC0846D40DF97EA CRC64;
 092406;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
 463 AA.
 145 AA.
 PRT;
 PRT;
 121 YGNYGVYAM-DYWGQGTSVTV 140
 PRELIMINARY;
 PRELIMINARY;
 145
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 STRAIN-C57BL/6;
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VTV 118
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 80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
 65 EWIGRIDPANGYTKYDPKFOGKATITADTSSNTAYLOLSSLTSEDTAVYFCAREGYYGNY 124
 3; Gaps
 6; Gaps
 20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
 5 WVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGL 64
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 52.1 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Ouery Match 57.5%; Score 429; DB 11; Length 481; Best Local Similarity 61.8%; Pred. No. 4.8e-34; Matches 84; Conservative 16; Mismatches 30; Indels 6
 21; Indels
 Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BF001490; AAH13490.1; -InterPro; IPR003006; Ig_MHC. Pfam; PF00047; 1g; 4. PROSITE; PS00290; IG_MHC; UNKNOWN_2. Hypothetical protein. SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 53.0 kDa protein.
 481 AA.
 488 AA
 13; Mismatches
 PRT;
 PRT;
 125 GVYAMDYWGQGTSVTV 140
 84; Conservative
 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID=10090;
 TISSUE-KIDNEY;
Strausberg R.;
 TISSUE-COLON;
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 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
 Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 .;
 Ouery Match 57.0%; Score 425.5; DB 11; Length 463; Best Local Similarity 59.3%; Pred. No. 1e-33; Matches 83; Conservative 21; Mismatches 33; Indels 3;
 Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1; -.
HSSP; P01842; 7FAB.
 Strausberg R;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013488; AAH13488.1;
MGD; MGT2144917; AI893585.
InterPro; IPR003598; Ig_C2.
InterPro; IPR003006; Ig_MHC.
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
 091WT3;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UJUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.0 kDa protein.
AI893585.
 PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein; Immunoglobulin domain.
 481 AA
 PRT;
 MGD; MGI:96446; Igh-4.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.C1.
InterPro; IPR003000; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR0047; Ig. 4.
 121 YGNYGVYAMDYWGQGTSVTV 140
 | :| ::| |||||| |||
121 Y-SYDLFA--YWGQGTLVTV 137
 PRELIMINARY;
 Pfam; PF00047; ig; 4. SMART; SM00408; IGc2; 1.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID=10090;
 TISSUE=COLON;
 Q91WT3
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 6, 2003, 12:46:55; Search time 24.6263 Seconds (without alignments) 573.557 Million cell updates/sec

Title: Perfect score:

US-09-155-739-7 562 1 DIOMIQSPSSLSASVGDRVT......YCLQYDNLWTFGQGTKVEIK 106 Sequence:

Scoring table:

908470 seqs, 133250620 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|            |   |        |                     |                    |                   |                   |                    |                    |                    |                    | •                  |                    |                    |
|------------|---|--------|---------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|            |   |        | Description         | Humanized anti-VLA | Humanised alpha-4 | Humanised alpha-4 | Mouse anti-VLA-4 a | Mouse VLA-4 antibo | Human VLA-4 reshap | Alpha-4 integrin m | Human MCP-3 and mu | Human IP-10 and mu | Artificial synthet |
| COLLACINOC |   |        | Ω                   |                    | AAW22412          | AAW22419          | AAR81328           | AAR81326           | AAR81332           | AAW22409           | AAY29913           | AAY29911           | AAY29916           |
|            |   |        | DB                  | 16                 | 18                | 18                | 16                 | 16                 | 16                 | 18                 | 20                 | 20                 | 20                 |
|            |   |        | e Match Length DB I | 106                | 106               | 126               | 106                | 126                | 126                | 126                | 359                | 361                | 374                |
|            | æ | Query  | Match               | 100.0              | 100.0             | 100.0             | 90.4               | 90.4               | 90.4               | 90.4               | 86.8               | 86.8               | 86.8               |
|            |   |        | Score               | 562                | 562               | 562               | 508                | 508                | 208                | 508                | 488                | 488                | 488                |
|            |   | Result | No.                 | 1                  | 7                 | m                 | 4                  | 2                  | 9                  | 7                  | 80                 | 6                  | 10                 |

| ,<br>ME1-14 light chain | ecifi    | æ        | Murine monoclonal | Variable region of | (FRP51)-ETA fusion | Anti-gp54 MAb T16 | ScFv(FWP51). Synt | sec      | Anti-gp54 MAb T16 | Humanized VLA-4 an | Humanised alpha-4 | Murine OKT4A light | FWP51 fusion prote | Human REI monoclon | Human/murine IL-1 | R. pipiens recombi | Variable Light dom | Humanised murine a | Humanised anti-VEG | ed li    | Anti-VEGF humanise | Humanised anti-VEG | CDR-gra  | ۲.       | isplay a | Variable Light dom | Humanised murine a | anti     | ō        | Human Vl consensus | an 1     | Human variable lig | Human consensus fr | Human consensus se |
|-------------------------|----------|----------|-------------------|--------------------|--------------------|-------------------|-------------------|----------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|----------|----------|----------|--------------------|--------------------|----------|----------|--------------------|----------|--------------------|--------------------|--------------------|
| AAR60627                | AAR13050 | AAR78970 | AAR93159          | AAR06252           | AAR26983           | AAW26797          | AAR85495          | AAY21882 | AAW26800          | AAR81322           | AAW22422          | AAR13658           | AAR26981           | AAR65163           | AAR47207          | AAW35133           | AAW86805           | AAW70625           | ABP61194           | AAW10231 | AAW70673           | ABP61242           | AAW10233 | AAW70703 | ABP61241 | Ö                  | AAW70623           | ABP61192 | AAW87455 | AAB62087           | AAB60400 | S                  | 7062               | 34                 |
| 15                      | 12       | 16       | 17                | 11                 | 13                 | 13                | 16                | 20       | 19                | 16                 | 18                | 12                 | 13                 | 16                 | 15                | 18                 | 19                 | 19                 | 23                 | 18       | 19                 | 23                 | 18       | 19       | 23       | 19                 | 19                 | 23       | 20       | 22                 | 22       | 22                 | 19                 | 21                 |
| 128                     | 234      | 107      | 108               | 128                | 637                | 109               | 240               | 241      | 245               | 107                | 107               | 109                | 241                | 108                | 129               | 355                | 107                | 107                | 107                | 108      | 110                | 110                | 234      | 237      | 650      | 107                | 107                | 107      | 107      | 107                | 107      | 107                | 108                | 108                |
|                         |          | -        |                   |                    |                    |                   | 81.0              |          |                   |                    |                   |                    |                    |                    |                   |                    |                    |                    |                    |          |                    |                    |          |          |          |                    |                    |          |          |                    |          |                    |                    |                    |
| 8                       | 75.      | ÷.       | 46                | ٠                  | 460                | 'n                | 455               | S        | S                 | 53.                | æ,                | S                  | S                  | •                  | ÷.                | S                  | 6                  | •                  | 49.                |          | •                  | •                  | 446.5    | •        | •        | ъ.                 | •                  | •        | 44.      | 44.                | 44.      | 444.5              | 44.                | 44.                |
| 11 .                    | . 12     | 13       | 14                | 15                 | 16                 | 17                | 18                | 19       | 20                | 21                 | 22                | 23                 | 24                 | 25                 | 26                | 27                 | 28                 | 29                 | 30                 | 31       | 32                 | 33                 | 34       | 35       | 36       | 37                 | 38                 | 39       | 40       | 41                 | 42       | 43                 | 44                 | 45                 |

## ALIGNMENTS

AAR81321

AAR81321 standard; Protein; 106 AA.

AAR81321;

02-APR-1996 (first entry)

Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic; Humanized anti-VLA-4 antibody 21.6 light chain variable region, La. THE STATE OF 
Chimeric Mus musculus. Chimeric Homo sapiens.

antibody engineering.

WO9519790-A1

27-JUL-1995.

25-JAN-1995; 95WO-US01219.

94US-0186269 25-JAN-1994;

(ATHE-) ATHENA NEUROSCIENCES INC.

Leger OJ, Saldanha J; Bendig MM, Jones TS,

WPI; 1995-269276/35.

New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.

N

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/note=
 /note=
 /note=
 Bendig MM, Jones ST,
 WPI; 1997-297879/27.
 Misc-difference 103
 Misc-difference 104
 Misc-difference 106
 69
 106 AA;
 Misc-difference
 Misc-difference
 WO9718838-A1
 21-NOV-1995;
 29-MAY-1997.
 Sequence
 Region
 Region
 Region
 Region
 variable region, La, directed against leukocyte adhesion molecule
variable region, La, directed against leukocyte adhesion molecule
VLA-4. Cloned CDNA sequences of mouse 21.6 VL and VH (AAQ99889 and
AAQ99892-1 regions are linked to human constant regions in the
construction of a humanized antibody against VLA-4. The 5' and 3'
ends of the mouse cDNAs are modified using PCR primers (See
AAQ99892-89) and then subcloned into mammalian cell expression vectors
containing human kappa or gamma-1 constant regions. In the humanized
light chain, amino acids L45, L58 and L69 in the humanized
containing human kappa or gamma-1.49, L58 and L69 in the humanized
light chain, amino acids L45, L58 and L69 in the humanized
containing human kappa or gamma-1.

VR framework are replaced by the amino acid present in the equivalent
position of the mouse 21.6 Ig L chain. Plasmids encoding the chimneric
antibodies are transfected into COS cells. The humanized antibodies
can be used for inhibiting adhesion of a leukocyte to an endothelial
cell and for treating inflammatory diseases such as multipp
cell and for treating inflammatory diseases such as multipp
cell and for treating inflammatory diseases such as multipp
cell acid for themingitis or encephalitis. The antibodies can
also be used for detecting VLA-4, for affinity purification or for
 ;
 0; Gaps
 The sequence encodes the humanized mouse antibody 21.6 light chain
 74.34
/label= CDR1
/note= "21.6 complementarity determining region 1"
 Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma: atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
 100.0%; Score 562; DB 16; Length 106; 100.0%; Pred. No. 1.2e-36; Live 0; Mismatches 0; Indels 0
 /note= "REI Lys-45 is substd. by Lys of mouse 21.6 VL, important in supporting the CDR2 loop"
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 Humanised alpha-4 integrin antibody 21.6 VL La.
 /label= FR1
/note= "RE1 framework region 1"
 'note= "REI framework region 2"
 generating anti-idiotype antibodies
 Location/Qualifiers
 AAW22412 standard; Protein; 106 AA.
 Claim 9; Page 67; 105pp; English.
 08-DEC-1997 (first entry)
 Matches 106; Conservative
 Chimeric Mus musculus;
Chimeric Homo sapiens;
Chimeric synthetic.
 Best Local Similarity
 106 AA;
 Misc-difference 49
 Misc-difference
 Sequence
 AAW22412;
 Query Match
 Key
Region
 Region
 Region
 RESULT 2
 AAW22412
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This polypoptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody and a modified human REI framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate fragments of mouse and human NAR sequences. The humanised 21.6 VL and a humanised 21.6 VL and a humanised 21.6 VL and be used
 to produce a claimed humanised 21.6 antibody that its useful in the manufacture of a medicament for treating asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, rheumatoid ischaemis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
 'note= "21.6 complementarity determining region 2"
 /note= "21.6 complementarity determining region 3"
 /note= "REI val-58 is substd. by Ile of mouse 21.6 VL, important in supporting the CDR2
 "REI Thr-106 substd. by Lys, more typical of human kappa light chain J region"
 /note= "REI Leu-103 substd. by Val, more typical of human kappa light chain J region"
 "REI Gln-104 substd. by Glu, more typical of human kappa light chain J region"
 Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
 "REI Thr-69 is substd. by Arg of mouse 21.6 VL, involved in antibody-antigen binding"
/note= "REI Tyr-49 is substd. by His of mouse 21.6 VL, located at the binding site"
 Leger OJ, Saldanha J, Yednock TA;
 57..88
/label= FR3
/note= "REI framework region 3"
 /note= "REI framework region 4"
 (ATHE-) ATHENA NEUROSCIENCES INC.
 Claim 25; Fig 6; 107pp; English.
 loop"
 /label= CDR2
 /label= CDR3
 95US-0561521.
 97..106
/label= 1
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 Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMIQSPSSLSASVGDRVITTCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 "21.6 complementarity determining region 1"
 /label= CDR3
/note= "21.6 complementarity determining region 3"
 "21.6 complementarity determining region 2"
 Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
 ö
 asthma; atheroscierosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rhemmatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
 Length 106;
 Saldanha J, Yednock TA;
 Indels
 RESGSGSGRDYTFISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 Humanised alpha-4 integrin antibody 21.6 VL version La.
 /label= Mat_protein
/note= "VL version La (Claim 25)"
100.0%; Score 562; DB 18;
100.0%; Pred. No. 1.2e-36;
live 0; Mismatches 0;
 "REI framework region 1"
 /label= FR4
/note= "RE1 framework region 4"
 /label- FR3
/note= "REI framework region 3"
 "REI framework region 2"
 Location/Qualifiers
 AAW22419 standard; Protein; 126 AA.
 Jones ST, Leger OJ,
 (ATHE-) ATHENA NEUROSCIENCES INC.
 /label- Leader
 /label= CDR2
 /label= CDR1
 950S-0561521
 96WO-US18807
 /label= FR1
 /label= FR2
 (first entry)
 116
 .126
 Conservative
 77..108
 Chimeric Mus musculus;
Chimeric Homo sapiens;
 /note=
 /note=
 Chimeric synthetic.
 Similarity
 21-NOV-1996;
 21-NOV-1995;
 WO9718838-A1
 08-DEC-1997
 29-MAY-1997
 Best Local Sim
Matches 106;
 Bendig MM,
 AAW22419;
 Query Match
 Peptide
 Protein
 Region
 Region
 Region
 Region
 Region
 Region
 Region
 61
 61
 RESULT 3
 AAW22419
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This polypeptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also AMV2412). It is composed of complementarity determining regions from the VL region (see AMV22409) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human REI framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate mouse and human DNA sequences. The humanised 21.6 VL and a humanised 21.6 VH (see AMV22413) can be used to produce a claimed humanised 21.6 antibody that is useful in the manufacture of a medicament for treating asthma, atherosclerosis, contrictis, transplant rejection, graft versus host disease, theumatic arthritis, transplant rejection, graft versus host disease, theumatic is claimed and acute leukocyte mediated lung injury. The humanised antibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
 Gaps
 1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 80
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
 /note= "mouse light chain variable complementarity determining region 1"
 /note= "mouse light chain variable complementarity determining region 2"
 ö
 Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
 100.0%; Score 562; DB 18; Length 126; 100.0%; Pred. No. 1.4e-36; Live 0; Mismatches 0; Indels 0
 /note= "mouse light chain variable framework
 /note= "mouse light chain variable framework
 Mouse anti-VLA-4 antibody 21.6 light chain variable region.
 Location/Qualifiers
 AAR81328 standard; Protein; 106 AA,
 Example 6; Fig 10; 107pp; English.
 region 1"
 region 2
 24..34
/label= CDR1
 /label= CDR2
 35..49
/label= FR2
 ...23
/label= FR1
 02-APR-1996 (first entry)
 Best Local Similarity 100.
Matches 106; Conservative
 antibody engineering.
 WPI; 1997-297879/27.
N-PSDB; AAT74788.
 Similarity
 126 AA;
 Aus musculus
 Sequence
 AAR81328;
 Query Match
 Key
Region
 Region
 Region
 Region
 RESULT 4
 AAR81328
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Mon Jan

23-MAR-1996 (first entry)

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The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain variable region (without signal sequence). Cloned cDNA CDR sequences of mouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the REI antibody for the light chain and the 2*CL antibody grainst VLA-4. The 5' and 3' ends of the mususe cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LCWR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig light contain the humanized antibodies are transfected into COS acid present in the equivalent position of the mouse 21.6 Ig light collair. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple solerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-diotype antibodies.
 ö
 Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 /note= "mouse light chain variable complementarity determining region 3"
 0;
 New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
 /note= "mouse light chain variable framework region 3"
 /note= "mouse light chain variable framework
region 4"
 jery Match 90.4%; Score 508; DB 16; Length 106; st Local Similarity 88.7%; Pred. No. 1.8e-32; tches 94; Conservative 6; Mismatches 6; Indels
 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 Saldanha J;
 Disclosure; Page 66; 105pp; English.
 (ATHE-) ATHENA NEUROSCIENCES INC.
 Bendig MM, Jones TS, Leger OJ,
 /label= CDR3
57..88
/label- FR3
 94US-0186269
 /label= FR4
 95WO-US01219
 901..76
 89..96
 inflammatory disease.
 WPI; 1995-269276/35.
 106 AA;
 WO9519790-A1
 25-JAN-1994;
 25-JAN-1995;
 27-JUL-1995.
 Seguence
 Query Match
 Region
 Region
 Region
 Matches
 61
 RESULT 5
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The sequence represents the mouse antibody 21.6 light chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned CDNA sequences of mouse 21.6 VL and VH (see AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids LA5, L49, L58 and L69 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 IL Chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and
 Gaps
 Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
 to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for
 ;
0
 "complementarity determining region 1"
 New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
 "complementarity determining region 2"
 "complementarity determining region 3"
 detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.
 90.4%; Score 508; DB 16; Length 126; 88.7%; Pred. No. 2.2e-32; Live 6; Mismatches 6; Indels
 Mouse VLA-4 antibody 21.6 light chain variable region.
 Leger OJ, Saldanha J;
 /note= "framework region 3"
 "framework region 1"
 "framework region 2"
 117..126
/note= "framework region 4"
 /note= "signal peptide"
 Location/Qualifiers
 Disclosure; Fig 1; 105pp; English.
 (ATHE-) ATHENA NEUROSCIENCES INC.
 95WO-US01219.
 94US-0186269.
 Query Match
Best Local Similarity 88.7;
Matches 94; Conservative
 /note=
117..12
 /note-
 /note=
 /note=
 /note=
 Bendig MM, Jones TS,
 antibody engineering.
 inflammatory disease.
 WPI; 1995-269276/35.
 126 AA;
 N-PSDB; AAQ99889
 WO9519790-A1.
 Mus musculus.
 25-JAN-1994;
 25-JAN-1995;
 27-JUL-1995.
 Sequence
 Peptide
 Region
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AAR81326 standard; Protein; 126 AA.

**AAR**81326

AAR81326

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21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
DIOMIQSPSSLSASVGDRVIITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
 chain variable region against leukocyte adhesion molecule VLA-4. Cloned CDNA sequences of mouse 21.6 VL (AAQ99889) and VH (AAQ9892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse CDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, anino acids LAS, LA9, LS8 and LS9 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent
 Human VLA-4 reshaped antibody 21.6 light chain variable region.
 The sequence represents the human reshaped antibody 21.6 light
 New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
 2
 "complementarity determining region 3"
 "complementarity determining region
 region
 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 /note= "complementarity determining
 Jones TS, Leger OJ, Saldanha J;
 ..108
note= "framework region 3"
 "framework region 1"
 117.126
/note= "framework region 4"
 "framework region 2"
 'note= "signal peptide"
 Location/Qualifiers
 Disclosure; Fig 10; 105pp; English.
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 (ATHE-) ATHENA NEUROSCIENCES INC.
 AAR81332 standard; Protein; 126
 95WO-US01219,
 94US-0186269.
 (first entry)
 ..116
 /note=
 /note=
 /note=
 'note=
 /note-
 antibody engineering.
 inflammatory disease.
 WPI; 1995-269276/35.
 N-PSDB; AAQ99893
 Homo sapiens
 WO9519790-A1
 25-JAN-1994;
 25-JAN-1995;
 23-MAR-1996
 27-JUL-1995,
 Bendig MM,
 AAR81332;
 Peptide
 Region
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 AAR81332
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Gaps
 1 DIQMTQSPSSLSASVGDRVT1TCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
 chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, menigitis or encephalitis. The antibodies can also be used for detecting VLA.4, for affinity purification or for generating anti-idlotype antibodies.
 Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
 ö
 asthma; atheroscierosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
 "complementarity determining region 1"
 /label= CDR3
/note= "complementarity determining region 3"
 Plasmids encoding the
 "complementarity determining region 2"
 Length 126;
 90.4%; Score 508; DB 16; Length 1
88.7%; Pred. No. 2.2e-32;
ive 6; Mismatches 6; Indels
 /note= "framework region 4"
 'note= "framework region 1"
 /note= "framework region 3"
 Alpha-4 integrin mouse MAb 21.6 VL region.
 "framework region
position of the mouse 21.6 Ig L chain.
 Location/Qualifiers
 AAW22409 standard; Protein; 126 AA.
 /label- Leader
 70..76
/label= CDR2
 14..54
/label= CDR1
 /label- FR3
 (first entry)
 Ouery Match
Best Local Similarity 88.77
Matches 94; Conservative
 117..126
/label= F
 55..69
/label= 1
 21..43
/label= :
 ..108
 'note=
 'note"
 126 AA;
 us musculus
 WO9718838-A1
 08-DEC-1997
 29-MAY-1997,
 Sequence
 AAW22409;
 Peptide
 Region
 Region
 Region
 Region
 Region
 Region
 Region
 Key
 RESULT 7
 AAW22409
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96WO-US18807.

21-NOV-1996;

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 Gaps
 21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine; immune response; HIV; infection.
 This polypeptide comprises the light chain variable region (VL) of mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VL can be incorporated into a human REI framework to produce a claimed humanised 21.6 VL (see AAW22412) and a claimed humanised 21.6 antibody that is used in the manufacture of a medicament for treating a disease selected from asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour metators.
 metastasis, nephritis, atopic dermattis, psoriasis, myocardial ischaemia, and acute leukcoyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin for use as a vaccine or an immunogen. It is also useful for expensiting idiotypic antibodies. The humanised antibodies of the quivention have a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
 .
0
 Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
 Length 126;
 Saldanha J, Yednock TA;
 6; Indels
 61 RFSGSGSCRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 90.4%; Score 50%; DB 18;
88.7%; Pred. No. 2.2e-32;
iive 6; Mismatches 6;
 Human MCP-3 and murine scFv38 fusion protein.
 (USSH) US DEPT HEALTH & HUMAN SERVICES.
 AAY29913 standard; Protein; 359 AA
 Claim 18; Page 68; 107pp; English.
 Bendig MM, Jones ST, Leger OJ,
 (ATHE-) ATHENA NEUROSCIENCES INC
 95US-0561521.
 98US-0077745.
 99WO-US05345
 17-NOV-1999 (first entry)
 94; Conservative
 WPI; 1997-297879/27.
 Best Local Similarity
 126 AA;
 N-PSDB; AAT74759
 21-NOV-1995;
 Homo sapiens.
 W09946392-A1
 12-MAR-1998;
 12-MAR-1999;
 16-SEP-1999.
 Mus sp.
Synthetic.
 Sequence
 AAY29913;
 Query Match
 Matches
 RESULT 8
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The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human Muc-1; (5) human IP-10 and HIV gpl20; (6) human MCP-3 and HIV gpl20; and (8) human SDF-1 and HIV gpl20; (7) human MDC and HIV gpl20; and (8) human SDF-1 and HIV gpl20. The fusion proteins, and nucleotide sequences encoding them, can be used for producing an immune response, e.g. an effector T cell immune preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays from identifying unknown tumour antigen epitopes and fine mapping of tumour antigen epitopes. The present sequence represents a fusion protein
 ó
 New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
 233 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLHYYSTLQPGIPS 292
 0; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
 DB 20; Length 359;
 7; Indels
 293 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLEIK 338
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 Score 488; DB 2(
Pred. No. 2e-30;
 Human IP-10 and murine scFv38 fusion protein.
 9; Mismatches
 Disclosure; Page 118–119; 142pp; English.
 (USSH) US DEPT HEALTH & HUMAN SERVICES.
 AAY29911 standard; Protein; 361 AA.
 immune response; HIV; infection
 86.8%;
84.9%;
 99WO-US05345.
 98US-0077745.
 (first entry)
 Query Match 86.8
Best Local Similarity 84.9
Matches 90; Conservative
Kwak LW, Biragyn A;
 WPI; 1999-551418/46.
 Kwak LW, Biragyn A;
 WPI; 1999-551418/46.
 359 AA;
 Homo sapiens.
 WO9946392-A1.
 12-MAR-1999;
 17-NOV-1999
 12-MAR-1998;
 16-SEP-1999.
 Mus sp.
Synthetic.
 infection
 AAY29911;
 Sequence
 RESULT 9
 AAY29911
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and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein:3 (MCP-3) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human interferon-induced chemokine (MDC) and human Muc-1; (4) human Muc-1; (5) human IP-10 and HIV gpl20; (6) human MCP-3 and human Muc-1; (5) human IP-10 and HIV gpl20; (6) human MCP-3 and human Muc-1; (7) human Muc-1; (6) human EP-10 and GP human SDF-1 and HIV gpl20; The fusion proteins, and nucleotide sequences encoding them, can be used for producing an immune response, e.g. an effector T cell fummune response. They can also be used for treating cancer or treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in or preventing assays for identifying unknown tumour antigen epitopes. ANZ21166 are sequences given in the SEQ ID LISTING in the present invention but which

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 The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human MCSP-1 and human Muc-1; (5) human IP-10 and HIV gpl20; (6) human MCP-3 and HIV gpl20; (7) human MCP-3 and HIV gpl20; (7) human MCP-3 and HIV gpl20; and (8) human MCP-3 and HIV gpl20. The fusion proteins, and nucleospose, e.g. an effector T cell immune be used for producing an immune response, e.g. an effector T cell immune response. They can also be used for treating cancer or treating or
 preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays torm identifying unknown tumour antigen epitopes and fine mapping of tumour antigen epitopes. The present sequence represents a fusion protein from the present invention.
New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
 235 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 294
 0; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 tumour; viral; antigen; fusion protein; cancer; vaccine;
 DB 20; Length 361;
 Indels
 Artificial synthetic construct protein SEQ ID NO:15.
 7;
 Score 488; DB 20
Pred. No. 2e-30;
9; Mismatches
 Disclosure; Page 115-116; 142pp; English.
 ¥.
 AAY29916 standard; Protein; 374
 immune response; HIV; infection
 86.8%;
 (first entry)
 Matches 90; Conservative
 Similarity
 361 AA;
 W09946392-A1
 17-NOV-1999
 16-SEP-1999
 Chemokine;
 Synthetic.
 infection
 AAY29916;
 Sequence
 Query Match
 Local
 RESULT 10
 AAY 2991
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Gaps 9

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7; Indels

Length 374;

Score 488; DB 20; Pred. No. 2.1e-30; 9; Mismatches

86.8%;

Ouery Match
Best Local Similarity 84.99
Matches 90; Conservative

are not mentioned further within the specification.

374 AA;

Seguence

95 DIQMIQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 154

g δλ

61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106

1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS

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 is
or
 The sequence is that of the MEI-14 light chain. The protein monoclonal antibody which can be administered to treat solid
 administering monoclonal antibody Mel-14, having Fc deleted, using injection or deposition in the cyst cavity
 Method of treating solid or cystic tumours with antibodies
155 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLEIK 200
 ME1-14 light chain variable region.
 Zalutsky MR;
 Š
 Disclosure; Fig 2; 31pp; English.
 AAR60627 standard; Protein; 128
 94WO-US02724.
 93US-0033864
 Monoclonal antibody; tumour
 04-JUN-1995 (first entry)
 Bigner DD, Carrel S,
 ZALUTSKY M R.
 BIGNER D D. CARREL S.
 WPI; 1994-316669/39
 See also AAR60626.
 N-PSDB; AAQ73537
 cystic tumours
 Homo sapiens.
 14-MAR-1994;
 19-MAR-1993;
 WO9421294-A.
 29-SEP-1994
 AAR60627;
 (BIGN/)
(CARR/)
 (ZALU/)
 RESULT 11
 AAR60627
 .
Db
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fusion polypeptides comprising a chemokine and a tumour antigen or antigen, used for treating cancers or treating or preventing HIV

(USSH ) US DEPT HEALTH & HUMAN SERVICES

Kwak LW, Biragyn A; WPI; 1999-551418/46.

99WO-US05345. 98US-0077745.

12-MAR-1999; 12-MAR-1998; The present invention describes fusion proteins comprising a chemokine

Disclosure; Page 117-118; 142pp; English.

infection

Page

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RESULT 13
AAR78970
 888888888888
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 Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 21 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLMHYTSTLQPGIPS 80
 New CD4 specific recombinant - complementarity determining region grafted antibody for treating graft rejection and T cell disorders
 ;
 Length 128;
 Jolliffe LK, Zivin RA, Pulito VL, Adair JR, Athwal DS;
 8; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 variable region; antibody; OKT4A; heavy chain; CD4; complementarity determining region.
 85.6%; Score 481; DB 15;
84.0%; Pred. No. 2.7e-30;
ive 9; Mismatches 8;
 133.,234
/label- kappa constant domain
 1..45
label= framework region 1
 77.110
/label= framework region 3
 'label= framework region 4

 3..69
 label= framework region

 ...20
'label= signal sequence
 CD4-specific CDR-grafted light chain.
 Location/Qualifiers
 AAR13050 standard; Protein; 234 AA.
 46..52
/label= CDR 1
 .0..76
'label= CDR 2
 .11..116
/label= CDR 3
 89GB-0028874.
90WO-GB02017.
90WO-GB02018.
 90WO-GB02015.
 27-SEP-1991 (first entry)
 Local Similarity 84.0 es 89; Conservative
 ..132
 (ORTH) ORTHO PHARM CORP.
 WPI; 1991-222914/30.
128 AA;
 N-PSDB; AAQ12633.
 21-DEC-1990;
 WO9109966-A.
 21-DEC-1989;
21-DEC-1990;
 21-DEC-1990;
 11-JUL-1991
Sequence
 Synthetic.
 AAR13050;
 Query Match
 Peptide
 Region
 Region
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Claim 1; Fig 8; 96pp; English,

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Hybridoma antibodies have been produced with the spleen cells of BALB/c mouse that had received multiple injections of mercuric ions reacted with glutathione to produce a mercuric ion coordinate covalent compound which was covalently bound to keyhole limpet hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5, 5B6 and 3E8) were producing Mabs that were strongly positive against glutatione-mercuric ions but negative against glutathione without mercuric ions. RNA was isolated from hybridoma cells with guanidine isothiocyanate. First strand cDNA synthesis was catalysed by MuLv reverse transcriptase. The primers used for cDNA synthesis were complementary to the 5' end of the CH1 domain of the heavy creat newscriptase. The primers used for cDNA synthesis are chain expressed by the hybridoma of interest, or to the 5' and of shown in AAQ97511-Q97518. The primer used for cDNA synthesis are
 New polypeptide(s) which bind heavy metals, esp. mercury - derived from monoclonal antibodies, used for detecting, removing, adding or
This is an example of a CDR-grafted light chain of the invention. The constant regions are based on sequences of the human kappa constant domain, the signal sequence is derived from murine MAD B72.3 and the CDR sequences are based on the murine OKT4A light chain CDRs. The recombinant antibody encoded by this sequence has affinity for CD4 similar to that of OKT4A.
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMTQSPSSLSASVGBRVTITCKASPDINNYLNWYQQTPGKAPKLLIYYTSTLQPGVPS 80
 1;
 DB 12; Length 234;
 Monoclonal antibody; heavy metal; mercury; variable region;
 84.6%; Score 475.5; DB 12; Length
84.9%; Pred. No. 1.3e-29;
ive 8; Mismatches 7; Indels
 Light chain variable region for monoclonal antibody 23F8.
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEI 105
 Claim 23; Page 67-68; 106pp; English.
 AAR78970 standard; Protein; 107 AA.
 Lopez O, Wagner FW, Wylie DE;
 94US-0187407.
 (first entry)
 Query Match
Best Local Similarity 84.99
Matches 90, Conservative
 neutralising heavy metals
 (BION-) BIONEBRASKA INC.
 WPI; 1995-275415/36.
N-PSDB; AAQ97508.
 234 AA;
 27-JAN-1994;
 27-JAN-1995;
 21-DEC-1995
 light chain.
 W09520607-A.
 03-AUG-1995.
 Synthetic.
 Sequence
 AAR78970;
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 for PCR amplification of that variable region, in conjunction with an appropriate V-region primer. In addition, the VH primer AAQ97518 was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences of the PCR amplified nucleotides were determined. These are given in AAQ97498-097510 and the deduced AA sequences in AAR9201-R79250 & AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45 sequence listings. The descriptions in the sequence listings are
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60
 CD29;
variable region of a particular antibody polypeptide was also used
 ä
 DB 16; Length 107;
 Antibody; light chain; kappa; variable region; K20; integrin; beta 1 subunit; humanisation; Hu-K20; immunosuppressant; T cell activation; complementarity determining region; CDR.
 Murine monoclonal antibody K20 kappa chain variable region.
 "complementarity determining region"
 "complementarity determining region"
 "complementarity determining region"
 Indels
 RFSGSGSGRDYTFISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
 Score 471.5; DB 16;
Pred. No. 1.3e-29;
9; Mismatches 8;
 (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 "framework region"
 "framework region"
 "framework region"
 Location/Qualifiers
 95..108
/label- J_kappa1
 AAR93159 standard; Protein; 108
 6
 83.9%;
 /label= CDR3
 4..34
'label= CDR1
 94FR-0010858
 94FR-0010858
 15..49
'label= FR2
 /label= FR3
 /label= FR1
 24-OCT-1996 (first entry)
 Conservative
 'label=
 note=
 /note=
 /note=
 Local Similarity
les 89; Conserv
 107 AA;
 FR2724393-A1
 12-SEP-1994;
 12-SEP-1994;
 Mus musculus
 15-MAR-1996
 Sequence
 AAR93159;
 Query Match
 Region
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 Region
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 Best Loc
Matches
 61
 RESULT 14
 AAR93159
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 8888888888888888
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Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 The present sequence is that of the variable region of the kappa light chain from murine monoclonal antibody K20. The antibody recognises the beta I subunit (CD29) of integrins and inhibits activation and proliferation of peripheral T cells induced by anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target for humanisation; the humanised version may be useful as an immunosuppressant. In the humanisation process, the complementarity determining regions (CDKS) of a human antibody with framework regions 70-95% homologous to those of K20 were replaced by the K20
 Expression vectors for producing chimeric monoclonal antibodies which express human constant region and non-human variable region
 Humanisation of non-human immunoglobulin variable regions - for prodn. of humanised antibodies, esp. K20, e.g. as an
 ö
 Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
 Length 108;
 Indels
 61 RFSGSGSCRDYSFSISNLEPEDIATYYCLQYYNLWTFGGGTKLEIK 106
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 Lefranc MP, Margaritte
 82.7%; Score 465; DB 17;
81.1%; Pred. No. 4.1e-29;
 Variable region of murine AHT 107 light chain.
 10; Mismatches
 AAR06252 standard; protein; 128 AA
(PROT-) PROTEINE PERFORMANCE SA.
 Example 1; Fig 2A; 39pp; French
 89US-0441702.
89US-0301216.
 90EP-0101351
 (MOLE-) MOLECULAR THERAPEU
 10-DEC-1990 (first entry)
 86; Conservative
 Cervoni MF,
 WPI; 1990-232892/31
 WPI; 1996-162083/17
 Similarity
 108 AA;
 immunosuppressant
 N-PSDB; AAQ05556
 N-PSDB; AAT26849
 24-JAN-1990;
 04-DEC-1989;
24-JAN-1989;
 01-AUG-1990
 EP380068-A.
 Bernard A,
 Sequence
 AAR06252
 Query Match
 Poul MA;
 Local
 Mus sp.
 Matches
 RESULT 15
 AAR06252
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1;
 Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Mabs comprising mouse CH and CL constant regions whith human variable regions may be used to create mouse/human hybrid Mabs, which have a longer serum half-life. Method can be used to produce Abs against interleukin-2 receptor and tumour necrosis factor.
 1;
 Ouery Match 81.9%; Score 460.5; DB 11; Length 128; Best Local Similarity 76.6%; Pred. No. 1.1e-28; Matches 82; Conservative 18; Mismatches 6; Indels 1;
 Search completed: January 6, 2003, 13:15:17
Job time : 25.6263 secs
 Disclosure; ; p; English.
 Sequence 128 AA;
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8 x 0 0 0 0 x 8
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6, 2003, 13:13:21 ; Search time 8.7798 Seconds
(without alignments)
355.228 Million cell updates/sec
 US-09-155-739-7
562
1 DIOMIQSPSSLSASVGDRVT......YCLQYDNLWTFGQGTKVEIK 106
 262574
 Issued_patents_AA:*
1: /cgn2_6/ptodatca1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodatca1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodatca1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodatca1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodatca1/iaa/pcruS_COMB.pep:*
6: /cgn2_6/ptodatca1/iaa/pcruS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 262574 seqs, 29422922 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 January
 Title:
Perfect score:
Sequence:
 Scoring table:
 Searched:
 Database
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|                     | Appli           | Appli            | Appli           | Appli            | Appli           | Appl             | Appli            | Appl              | Appli           | Appl             | Appl             | Appl              | Appl             |                   |                  | Appli           | Appli            | Appl             | Appl              | Appl              | Appl              | Appl              | Appl              | Appl              | Appl              | Appl              | Appli           |
|---------------------|-----------------|------------------|-----------------|------------------|-----------------|------------------|------------------|-------------------|-----------------|------------------|------------------|-------------------|------------------|-------------------|------------------|-----------------|------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|
| 2                   | 1,              | 7,               | 5,              | 2                | 7               | 15,              | 2,               | 15,               | 4,              | 22,              | 16,              | 16,               | 11,              | 11,               | 29,              | 8               | 8                | 57,              | 17,               | 17,               | 17,               | 17,               | 18,               | 18,               | 18,               | 18,               | 3,              |
| Description         | Sequence        | Sequence         | Sequence        | Sequence         | Sequence        | Sequence         | Sequence         | Sequence          | Sequence        | Sequence         | Sequence         | Sequence          | Sequence         | Sequence          | Sequence         | Sequence        | Sednence         | Sequence         | Sequence          | Sequence          | Sequence          | Sequence          | Sequence          | Sequence          | Sequence          | Sequence          |                 |
| ΔΙ                  | US-08-561-521-7 | PCT-US95-01219-7 | US-08-561-521-5 | PCT-US95-01219-5 | US-08-561-521-2 | US-08-561-521-15 | PCT-US95-01219-2 | PCT-US95-01219-15 | US-08-339-582-4 | US-08-888-366-22 | US-08-235-838-16 | US-08-465-473B-16 | US-08-235-838-11 | US-08-465-473B-11 | US-08-602-725-29 | US-08-561-521-8 | PCT-US95-01219-8 | US-08-875-811-57 | US-07-934-373C-17 | US-08-437-642B-17 | US-08-146-206C-17 | PCT-US93-07832-17 | US-07-934-373C-18 | US-08-437-642B-18 | US-08-146-206C-18 | PCT-US93-07832-18 | US-08-974-899-3 |
| DB                  | 7               | ហ                | ~               | Ŋ                | 7               | 7                | 2                | Ŋ                 | Н               | ~                | ч                | ~                 | -                | 7                 | 7                | 7               | Ŋ                | m                | 7                 | m                 | 4                 | Ŋ                 | 7                 | m                 | 4                 | S                 | m               |
| Length              | 106             | 106              | 106             | 106              | 126             | 126              | 126              | 126               | 128             | 107              | 637              | 637               | 241              | 241               | 108              | 107             | 107              | 355              | 107               | 107               | 107               | 107               | 107               | 107               | 107               | 107               | 108             |
| %<br>Query<br>Match | 100.0           | 100.0            | 90.4            | 90.4             | 90.4            | 90.4             | 90.4             | 90.4              | 85.6            | 83.9             | 81.9             | 81.9              | 81.0             | 81.0              | 80.9             | 80.7            | 80.7             | 80.2             | 79.8              | 79.8              | 79.8              | 79.8              | 79.1              | 79.1              | 79.1              | 79.1              | 79.1            |
| Score               | 562             | 295              | 208             | 508              | 508             | 508              | 508              | 508               | 481             | 471.5            | 460              | 460               | 455              | 455               | 454.5            | 453.5           | 453.5            | 451              | 448.5             | 448.5             | 48                | m                 | 444.5             | 444.5             | 444.5             | 444.5             | 444.5           |
| Result<br>No.       | 1               | 7                | m               | 4                | 'n              | 9                | 7                | 89                | 6               | 10               | 11               | 12                | 13               | 14                | 15               | 16              | 17               | 18               | 19                | 20                | 21                | 22                | 23                | 24                | 25                | 56                | 27              |

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-------------------------------------------------------------------------------------------------------------------------|--------------------------------------------|
| 677, 711, 711, 711, 711, 711, 711, 711,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                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US-08-137-117D-67<br>US-08-436-717-67<br>US-08-437-117D-71<br>US-08-561-521-6<br>US-08-652-528-34<br>US-09-652-528-34<br>US-09-052-023-15<br>PCT-US95-01219-6<br>US-08-116-247-9<br>US-08-318-157B-6<br>US-08-318-157B-6<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-558-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-652-58-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68-2<br>US-08-68- 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No. 1.2<br>Mismatches    |
| 08-137<br>08-436<br>08-137<br>08-551<br>08-551<br>08-561<br>09-025<br>09-025<br>09-07-934<br>08-116<br>08-116<br>08-116<br>08-116<br>08-116<br>08-116<br>08-117<br>08-117<br>08-117<br>08-117<br>08-117                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                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N<br>Misma                |
| 08-<br>08-<br>08-<br>08-<br>08-<br>08-<br>08-<br>08-<br>08-<br>08-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | AL.  //08561521  y M. ier J. ose are J. ose and Townse laza, Steu and Townse laza, Steu  | ć                                          |
| 101000400000004000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | IS/0856 IS/0856 ITY M. Vier J Jose Jose Jose Jose Jose Jose Jose Jos                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 8.6                                        |
| 1111<br>1111<br>126<br>126<br>107<br>107<br>108<br>109<br>109<br>109<br>109<br>109                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | on had on on the control of the cont | 100.0%;<br>larity 100.0%;<br>Conservative  |
| 79.1<br>79.1<br>79.1<br>79.1<br>78.9<br>78.9<br>78.4<br>78.4<br>78.4<br>78.4<br>78.4<br>78.4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ULT 1  O8-561-521-7  equence 7, Application U atent No. 5840299  GENERAL INFORMATION: APPLICANT: Bendig, Ma APPLICANT: Leger, Oli- APPLICANT: Saldanha, APPLICATION: H  CORRESPONDENCES: CORRESPONDENCE ADDRESS ADDRESSEE: Townsend STREET: One Market CITY: San Francisco STREET: One Market CITY: San Francisco STREET: One Market CITY: 94105  COMPUTER READALE FORM MEDIUM TYPE: FLOPPY MEDIUM TYPE: PLOPPY APPLICATION NUMBER: FILING DATE: CLASSIFICATION DATA APPLICATION NUMBER: FILING DATE: FILING DATE: 25-JAN ATORNEY, AGENT INFORMA NAME: SMITH, NUMBER: REFERRNC-FOCKET NUM TELECHMONE: 415-543-50 INFORMATION FOR SEQ ID M SEQUENCE CHARACTERISTI LENGTH: 106 amino at TYPE: TYPE: amino acid STRANDEDNESS: singl. TYPE: amino acid STRANDEDNESS: singl. TOPOLCGY: linear MOLECULE TYPE: protein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ch<br>1 Similarity<br>106; Conser          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Applicable  | EH .                                       |
| 4444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | THE STATE OF THE S | 3h<br>106.                                 |
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GENERAL INFORMATION:
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 0; Gaps . 0;
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 100.0%; Score 562; DB 5; Length 106; 100.0%; Pred. No. 1.2e-45; Live 0; Mismatches 0; Indels (
 APPLICANT: Bendig, Mary M.
APPLICANT: Beger, Olivier J.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SOUENCES: 45
CORRESPONDENCE S.
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/01219
 APPLICATION DAMBER: US. 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGCET INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 18-543-9600
 WWBER: PCT/US95/01219
25-JAN-1995
 Sequence 7, Application PC/TUS9501219 GENERAL INFORMATION:
 OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 5, Application US/08561521
Patent No. 5840299
 IBM PC compatible
 TELEFRAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 7:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
 Matches 106; Conservative
 SEQUENCE CHARACTERISTICS:
 CLASSIFICATION:
PRIOR APPLICATION DATA:
 TOPOLOGY: linear MOLECULE TYPE: protein PCT-US95-01219-7
 CITY: San Francisco
STATE: California
 Similarity
 USA
 FILING DATE:
 94105
 COMPUTER:
 PCT-US95-01219-7
 COUNTRY:
 US-08-561-521-5
 Query Match
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 1 DIQMIQSPSSLSASLGGKVTITCKTSQDINKYWAWYQHKPGKRPRLLIHYTSALQPGIPS 60
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
 Sequence 5, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Ollvier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
 Length 106;
 90.4%; Score 508; DB 2; Length 10
88.7%; Pred. No. 1.3e-40;
ive 6; Mismatches 6; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
 ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 SITATE: San Francisco SITATE: Callfornia
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILLING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
 15270-14
 NAME: Smith, William L. REGISTRATION NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 15;
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
 TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 5:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
 Matches 94; Conservative
 single
 TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-5
 CITY: San Francisco STATE: California COUNTRY: USA
 TYPE: amino acid
STRANDEDNESS: sin
 Similarity
 COUNTRY: USA
 FILING DATE:
 94105
 RESULT 4
PCT-US95-01219-5
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
 Query Match
Best Local Similarity 88.75
Matches 94; Conservative
 SEQUENCE CHARACTERISTICS:
 TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-2
 TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-15
 STREET: One Market P
CITY: San Francisco
STATE: California
 USA
 ZIP: 94105
 COUNTRY:
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 0; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 APPLICANT: Bendig, Mary M.
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
 Length 106;
 6; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 61 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106
 E: Townsend and Townsend Khourie and Crew
One Market Plaza, Steuart Tower, Suite 2000
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
 Query Match 90.4%; Score 508; DB 5; Best Local Similarity 88.7%; Pred. No. 1.3e-40; Matches 94; Conservative 6; Mismatches 6;
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/186,269
FILING DATE: 25-7AN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 15270-14
TELECHONE: 415-543-9600
TELECHONE: 415-543-9600
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
 ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 RESULT 5
US-08-561-521-2
IS-08-561-521-2
; Sequence 2. Application US/08561521
; Patent No. 5840799
; GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 106 amino acids TYPE: amino acid STRANDEDNESS: single
 TOPOLOGY: linear
MOLECULE TYPE: protein
 STREET: One Market P
CITY: San Francisco
STATE: California
 USA
 FILING DATE:
 ADDRESSEE:
 PCT-US95-01219-5
 COUNTRY:
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 Gaps
 21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 ö
 APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
 Score 508; DB 2; Length 126; Pred. No. 1.6e-40;
 6; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 OFFIGATIONG SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 90.4%; Sco...
88.7%; Pred. No. 1...
6; Mismatches
 CURRENT AFFLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFECATION: 424
PROOF APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN 1994
ATOMEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 15270-14
 US-08-561-521-15; Sequence 15, Application US/08561521 Patent No. 5640299; GENERAL INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
NAME: Smith, William L. REGISTRATION NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 15;
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
 INFORMATION FOR SEQ ID NO: 15:
 TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
 : 126 amino acids
amino acid
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PCT-US95-01219-15
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 0; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
 Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMTQSPSSLSASILGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
 0;
 90.4%; Score 508; DB 2; Length 126; 88.7%; Pred. No. 1.6e-40; Live 6; Mismatches 6; Indels
 TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS:
 Query Match 90.4%; Score 508; DB 5; Length 126; Best Local Similarity 88.7%; Pred. No. 1.6e-40; Matches 94; Conservative 6; Mismatches 6; Indels
 61 RFSGSGSGRDYTFIISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 2000
 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
 15270-14
 Sequence 2, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
 PC-DOS/MS-DOS
 COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
 30,223
 APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
 INFORMATION FOR SEQ ID NO: 2:
 NAME: Smith, William L. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
 LENGTH: 126 amino acids TYPE: amino acid
 Query Match
Best Local Similarity 88.79
Matches 94; Conservative
 TELEFAX: 415-543-5043
 SEQUENCE CHARACTERISTICS
 MOLECULE TYPE: protein
 San Francisco
: California
 linear
 FILING DATE: 25 CLASSIFICATION:
 IISA
 94105
 ADDRESSEE:
 TOPOLOGY:
 RESULT 7
PCT-US95-01219-2
 PCT-US95-01219-2
 COUNTRY:
 STATE:
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RESULT 8

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0; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLHHYTSALQPGIPS 80
Sequence 15, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
 Query Match
90.4%; Score 508; DB 5; Length 126;
Best Local Similarity 88.7%; Pred. No. 1.6e-40;
Matches 94; Conservative 6; Mismatches 6; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
 APPLICANT: Bigner, Darell D.
APPLICANT: Zalutsky, Michael R.
APPLICANT: Carrel, Stefan
TITLE OF INVENTION: METHOD OF TREATMENT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TLING DATE: 25-7AN-1994
ATTORNEY/AGENT INFORMATION:
NAME: SMICH, WILLIAM L.
RESISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECHONE: 415-543-9600
TELEFAX: 415-543-9603
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 4, Application US/08339582
Patent No. 5558852
GENERAL INFORMATION:
 ADDRESSEE: Kenneth D. Sibley
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 5558852th Carolina
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 INFORMATION FOR SEQ ID NO: 15:
 LENGTH: 126 amino acids TYPE: amino acid
 SEQUENCE CHARACTERISTICS:
 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-15
 NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
 USA
 USA
 COUNTRY: US
 STATE: NC
COUNTRY:
 US-08-339-582-4
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Mon Jan

us-09-155-739-7.rai

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Gaps
 APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina Maria
APPLICANT: Hardman, No. 5571894man
APPLICANT: Hardman, No. 5571894man
APPLICANT: Hardman, No. 5571894man
APPLICANT: Hardman, No. 5571894man
APPLICANT: Azickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Prince
 DB 2; Length 107;
 Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/235,838
 Score 471.5; DB 2;
Pred. No. 3.4e-37;
 83.2%; Scc. No. ...
83.2%; Pred. No. ...
9; Mismatches
 APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTORNEY, FAGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.39USC1
TELECOMMUNICATION INFORMATION:
TELEFHONE: 612-332-530
 FILING DATE: TBA
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION UNTAR:
APPLICATION UNBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
 Sequence 16, Application US/08235838
Patent No. 5571894
GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
 INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: LENGTH: 107 amino acids TYPE: amino acid
 NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
 89; Conservative
 , MOLECULE TYPE: protein US-08-888-366-22
 linear
 Query Match
Best Local Similarity
 CITY: Hawthorne STATE: New York
 USA
 COUNTRY: US
 TOPOLOGY:
 US-08-235-838-16
 Matches
 RESULT 11
 δ
 Sequence 22, Application US/08888366
Patent No. 5972656
GENERAL INFORMATION:
APPLICANT: Lopez, Osvaldo
APPLICANT: Wajle, Dwane E.
APPLICANT: Wajne, Pred W.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
CORRESPONDENCE ADDRESS:
 ö
 0; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMTQSPSSLSASILGGKVTITCKASQDINKYIAWYQHKPGKGPRLLMHYTSTLQPGIPS 80
 Length 128;
 ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr
STATE: Minneapolis
STATE: MA
 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/088,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,582
 / Match 85.6%; Score 481; DB 1; L
Local Similarity 84.0%; Pred. No. 5.3e-38;
Nes 89; Conservative 9; Mismatches 8;
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 08/033,864
FILING DATE: 19-MAR-1993
ATTORNEY_AGENT INFORMATION:
NAME: Sibley, Kennech D.
RECISTRATION NUMBER: 31,665
REFERENCE_DOCKET NUMBER: 5405-89
TELECHONE: 919-420-2200
TELEFAX: 919-881-3175
ZIP: 28234
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 TELEFAX: 919-881-3175 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
 ; MOLECULE TYPE: protein US-08-339-582-4
 ZIP: 55402
COMPUTER READABLE FORM:
 linear
 USA
 FILING DATE:
 TOPOLOGY:
 US-08-888-366-22
 COUNTRY:
 Query Match
 Best Loca
Matches
 RESULT 10
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; MOLECULE TYPE: protein US-08-465-473B-16
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 168 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 227
 0; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 81.9%; Score 460; DB 1; Length 637;
80.2%; Pred. No. 2.8e-35;
Live 10; Mismatches 11; Indels
 TITLE OF INVENTION: Recombinant Antibodies Specific for a TITLE OF INVENTION: Growth Factor Receptor
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 228 RFSGSGSGRDYSFSIHNLEPEDIATYXCLHYDYLYTFGGGTKLEIK 273
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
FILING DATE: 5 June 1995
REPERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8669
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
TELENTH: 637 amino acids
TYPE: amino acid
 4-18518/A/CIP/CONT2
 CLASSIFICATION: 4.2.
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J.
AA-18518/A/
 Sequence 16, Application US/08465473B
Patent No. 593931
GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5939531man
APPLICANT: Zwickl, Markus
 NOVARTIS Corporation
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
 TELEFAX: (908)522 6955
NFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: amino acid
 564 Morris Avenue
 Query Match
Best Local Similarity 80.28
Matches 85; Conservative
 MOLECULE TYPE: protein
 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
 New Jersey
 linear
 COUNTRY: USA
ZIP: 07901-6940
 TOPOLOGY: linear
 US-08-465-473B-16
 ADDRESSEE:
 US-08-235-838-16
 TOPOLOGY:
 STREET:
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 0; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 0; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Length 637;
 Length 241;
 Ouery Match 81.0%; Score 455; DB 1; Length 24; Best Local Similarity 80.0%; Pred. No. 2.8e-35; Matches 84; Conservative 10; Mismatches 11; Indels
 APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Ardman, No. 5571894man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
 11; Indels
 228 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,838
FILING DATE: TBA
CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-3AN-1992
FILING DATE: 31-3AN-1992
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
RELIGION NUMBER: GB 91-810079.3
FILING DATE: O5-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,1295
Query Match
81.9%; Score 460; DB 2;
Best Local Similarity 80.2%; Pred. No. 2.8e-35;
Matches 85; Conservative 10; Mismatches 11
 REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
TELECOMUNICATION INFORMATION:
TELEPHONE: (919)341-8614
 10; Mismatches
 CIBA-GEIGY Corporation
 Sequence 11, Application US/08235838 Patent No. 5571894 GENERAL INFORMATION:
 APPLICANT: Wels, Winfried S. APPLICANT: Hynes, Nancy E.
 TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 11:
 ADDRESSES: CIBA-GELO. C. STREET: 7 Skyline Drive CITY: Hawthorne STAIE: New York
 LENGTH: 241 amino acids TYPE: amino acid
 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-235-838-11
 US-08-235-838-11
```

```
APPLICANT: DURBIN, HELGA
APPLICANT: SNARY, DAVID
APPLICANT: STEWART, LORNA MD
APPLICANT: STEWART, LORNA MD
APPLICANT: YOUNG, SUSAN
APPLICANT: BATES, PAUL A
TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
 COMPUTER EAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC COMPUTER:
COMPUTER: TBM PC COMPUTER:
COMPUTER: TBM PC COMPUTER:
COMPUTER: TBM PC COMPUTER:
APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01816
FILING DATE: 19-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01816
FILING DATE: 21-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 3663
REFERENCE/DOCKET NUMBER: 3663
TELEFAX: 703-816-4100
TELEFAX: 703-816-4100
 ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
 Search completed: January 6, 2003, 13:19:09 Job time: 9.7798 secs
 ; ORGANISM: Hukan REI light chain US-08-602-725-29
Sequence 29, Application US/08602725
Patent No. 5965710
GENERAL INFORMATION:
APPLICANT: BODMER, WALTER F
 TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
 nrPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
 LENGTH: 108 amino acids
 MOLECULE TYPE: peptide HYPOTHETICAL: NO
 single
 linear
 amino acid
 CITY: ARLINGTON STATE: VA
 USA
 STRANDEDNESS:
 22201
 TOPOLOGY:
 COUNTRY:
 a
 ö
137 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 196
 Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 ö
 Sequence 11, Application US/08465473B
Patent No. 5939531
GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Hardman, No. 5939531man
APPLICANT: Hardman, No. 5939531man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
 Query Match 81.0%; Score 455; DB 2; Length 241; Best Local Similarity 80.0%; Pred. No. 2.8e-35; Matches 84; Conservative 10; Mismatches 11; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEI 105
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEI 105
 OFTAKALING SISLEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
FILING DATE: 5 June 1995
CLASSIFICATION ATA:
FILING DATE: 31-3AN-1992
PRIOR APPLICATION DATA:
THING DATE: 31-3AN-1992
PRIOR APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-3AN-1992
PRIOR APPLICATION NUMBER: US 07/828,832
FILING DATE: 05-FEB-1991
ATFORNEY/AGENT INFORMATION:
NAME: Pfelffer, Hesna J.
REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 22,640
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: (908)522 6940
 STATE: New Jersey
COUNTRY: USA
ZIP: 07901-6940
COMPUTER READABLE FORM:
WEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS Corporation
 TELEFAX: (908)522 6955
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
 564 Morris Avenue
 ; MOLECULE TYPE: protein US-08-465-473B-11
 TYPE: amino acid
TOPOLOGY: linear
 CITY: Summit
STATE: New Je
 RESULT 14
US-08-465-473B-11
 RESULT 15
US-08-602-725-29
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 1; Gaps
 Query Match 80.9%; Score 454.5; DB 2; Length 108; Best Local Similarity 83.0%; Pred. No. 1.3e-35; Matches 88; Conservative 8; Mismatches 9; Indels 1;
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: \cgn2_6/ptodata/2/pubpaa/US0B_NEW_PUB.pep:*
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 117078 seqs, 18951520 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
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 Minimum DB seq length: 0
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 US-09-155-739-7
 January
 Title:
Perfect score:
 Scoring table:
 Database :
 Sequence:
 Searched:
 Run on:
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## SUMMARIES

| 117               | 15.                                        | Sequence 16, Appl                                              | Sequence 15, Appl                                                                                                                      | Sequence 103, App                                                                                                                                                                    | Sequence 100, App                                                                                                                                                                                                     | Sequence 2, Appli                                                                                                                                                                                                                                                     | Sequence 13, Appl                                                                                                                                                                                                                                                                                              | Sequence 12, Appl                                                                                                                                                                                                                                                                                                                             | Sequence 6, Appli                                                                                                                                                                                                                                                                                                                                                                     | Sequence 15, Appl                                    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Sequence 15, Appl                                                                                                                                                                                                                                                                                                                                                                                                         | •                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            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US-09-229-200A-15 Sequence 15, 83.0 108 10 US-09-229-200A-16 Sequence 16, 80.0 107 10 US-09-056-160B-15 Sequence 16, 79.4 110 10 US-09-056-160B-103 Sequence 103, 79.4 237 10 US-09-056-160B-103 Sequence 100, 79.4 491 2 US-10-011-125-2 Sequence 2, A | 85.3 108 10 US-09-229-200A-11 Sequence<br>85.3 108 10 US-09-229-200A-15 Sequence<br>83.0 108 10 US-09-229-200A-16 Sequence<br>80.0 107 10 US-09-056-160B-15 Sequence<br>79.4 110 10 US-09-056-160B-100 Sequence<br>79.4 491 12 US-10-011-125-2 Sequence<br>79.3 107 10 US-09-056-160B-100 Sequence<br>79.3 107 10 US-09-056-160B-100 Sequence | 85.3 108 10 US-09-229-200A-11 Sequence<br>85.3 108 10 US-09-229-200A-15 Sequence<br>83.0 108 10 US-09-229-200A-16 Sequence<br>80.0 107 10 US-09-056-160B-15 Sequence<br>79.4 10 10 US-09-056-160B-103 Sequence<br>79.4 237 10 US-09-056-160B-103 Sequence<br>79.4 491 12 US-10-011-125-2 Sequence<br>79.1 108 10 US-09-056-160B-13 Sequence<br>79.1 108 10 US-09-056-160B-12 Sequence | 85.3 108 10 US-09-229-200A-11 Sequence 11, 85.3 108 10 US-09-229-200A-15 Sequence 15, 80.0 107 10 US-09-229-200A-16 Sequence 15, 80.0 107 10 US-09-056-160B-15 Sequence 16, 79.4 237 10 US-09-056-160B-103 Sequence 100, 79.4 491 12 US-10-011-125-2 Sequence 2, A 79.3 107 10 US-09-056-160B-13 Sequence 2, A 79.1 108 10 US-09-056-160B-13 Sequence 2, A 79.1 108 10 US-09-056-160B-12 Sequence 12, 79.1 108 10 US-09-056-160B-12 Sequence 6, A 79.1 109 10 US-09-056-160B-12 Sequence 12, A 79.1 109 10 US-09-056-160B-12 Sequence 6, A 79.1 109 10 US-09-056-160B-12 Sequence 6, A 79.1 109 10 US-09-056-160B-12 Sequence 12, A 79.1 109 10 US-09-056-160B-12 Sequence 12, A 79.1 100 US-09- | 85.3 108 10 US-09-229-200A-11 Sequence<br>85.3 108 10 US-09-229-200A-15 Sequence<br>83.0 108 10 US-09-269-200A-15 Sequence<br>80.0 107 10 US-09-056-160B-103 Sequence<br>79.4 237 10 US-09-056-160B-100 Sequence<br>79.4 491 12 US-10-011-125-2 Sequence<br>79.3 107 10 US-09-056-160B-13 Sequence<br>79.1 109 10 US-09-911-123-6 Sequence<br>79.1 109 10 US-09-911-123-6 Sequence<br>78.9 107 9 US-09-911-123-6 Sequence | 85.3 108 10 US-09-229-200A-11 Sequence 85.3 108 10 US-09-229-200A-15 Sequence 83.0 108 10 US-09-229-200A-15 Sequence 80.0 107 10 US-09-056-160B-15 Sequence 79.4 110 10 US-09-056-160B-103 Sequence 79.4 491 12 US-101-125-2 Sequence 79.3 107 10 US-09-056-160B-12 Sequence 79.1 108 10 US-09-056-160B-12 Sequence 79.1 108 10 US-09-056-160B-12 Sequence 79.1 109 10 US-09-059-025-15 Sequence 178.9 107 9 US-09-999-025-15 Sequence 178.9 107 9 US-09-999-040-15 | 85.3 108 10 US-09-229-200A-11 Sequence 85.3 108 10 US-09-229-200A-15 Sequence 83.0 108 10 US-09-229-200A-15 Sequence 80.0 107 10 US-09-056-160B-15 Sequence 79.4 10 10 US-09-056-160B-103 Sequence 79.4 237 10 US-09-056-160B-103 Sequence 79.4 491 12 US-10-011-125-2 Sequence 79.3 107 10 US-09-056-160B-12 Sequence 79.1 108 10 US-09-056-160B-12 Sequence 79.1 109 10 US-09-056-160B-12 Sequence 79.1 109 10 US-09-911-123-6 Sequence 79.1 109 10 US-09-999-025-15 Sequence 78.9 107 9 US-09-999-040-15 Sequence 78.9 107 9 US-09-999-040-15 Sequence 78.9 108 10 US-09-904-015 Sequence 78.9 108 10 US-09-292-200A-14 Sequence 78.9 108 10 US-09-292-200A-14 Sequence | 108 10 US-09-229-200A-11 Sequence 108 10 US-09-229-200A-15 Sequence 108 10 US-09-229-200A-15 Sequence 108 10 US-09-229-200A-15 Sequence 110 10 US-09-056-160B-103 Sequence 237 10 US-09-056-160B-103 Sequence 237 10 US-09-056-160B-103 Sequence 107 10 US-09-056-160B-13 Sequence 107 10 US-09-099-025-15 Sequence 1109 10 US-09-999-025-15 Sequence 1107 9 US-09-999-025-15 Sequence 1107 9 US-09-999-025-15 Sequence 1108 10 US-09-999-025-15 Sequence 1108 10 US-09-999-025-15 Sequence 1100 10 US-09-920-00A-15 Sequence 1100 10 US-09-920-00A-14 Sequence 1100 10 US-09-056-160B-105 Sequence 1100 US-09-056-160B-105 Sequence 1100 10 US-09-056-160B-105 Sequence 1100 US-09-056-160B-105 Sequence 1100 US-09-056-160B-105 Sequence | 85.3 108 10 US-09-229-200A-11 Sequence 85.3 108 10 US-09-229-200A-15 Sequence 83.0 108 10 US-09-229-200A-15 Sequence 80.0 107 10 US-09-056-160B-15 Sequence 79.4 110 10 US-09-056-160B-103 Sequence 79.4 491 12 US-10-011-125-2 Sequence 79.3 107 10 US-09-056-160B-103 Sequence 79.3 107 10 US-09-056-160B-12 Sequence 79.1 109 10 US-09-098-125-15 Sequence 79.1 109 10 US-09-99-025-15 Sequence 78.9 107 9 US-09-999-040-15 Sequence 78.9 109 10 US-09-929-200A-14 Sequence 178.9 109 100 US-09-929-200A-14 Sequence 178.9 109 10 US-09-929-200A-14 Seq | 85.3 108 10 US-09-229-200A-11 Sequence 85.3 108 10 US-09-229-200A-15 Sequence 80.0 108 10 US-09-229-200A-15 Sequence 80.0 107 10 US-09-056-160B-15 Sequence 79.4 10 10 US-09-056-160B-103 Sequence 79.4 491 12 US-010-01-125-2 Sequence 79.3 107 10 US-09-056-160B-12 Sequence 79.1 108 10 US-09-056-160B-12 Sequence 79.1 108 10 US-09-056-160B-12 Sequence 79.1 109 10 US-09-999-0025-15 Sequence 78.9 107 9 US-09-999-0025-15 Sequence 78.9 107 9 US-09-999-0026-160B-10 Sequence 78.9 108 10 US-09-999-0040-15 Sequence 78.9 108 10 US-09-992-200A-14 Sequence 78.9 109 10 US-09-922-200A-7 Sequence 78.7 108 9 US-10-153-159-2 Sequence 78.7 108 0 US-10-153- | 85.3 108 10 US-09-229-200A-11 Sequence 85.3 108 10 US-09-229-200A-15 Sequence 80.0 107 10 US-09-229-200A-15 Sequence 80.0 107 10 US-09-056-160B-105 Sequence 79.4 237 10 US-09-056-160B-100 Sequence 79.4 237 10 US-09-056-160B-100 Sequence 79.3 107 10 US-09-056-160B-12 Sequence 79.1 108 10 US-09-056-160B-12 Sequence 79.1 108 10 US-09-056-160B-12 Sequence 78.9 107 9 US-09-999-040-15 Sequence 78.9 107 9 US-09-999-040-15 Sequence 78.9 108 10 US-09-229-200A-14 Sequence 78.9 108 10 US-09-229-200A-7 Sequence 78.9 108 10 US-09-229-200A-7 Sequence 78.9 108 10 US-09-229-200A-7 Sequence 78.7 108 9 US-10-153-159-16 Sequence 178.7 108 9 US-10-153-159 | 85.3 108 10 US-09-229-200A-11 Sequence 85.3 108 10 US-09-229-200A-15 Sequence 80.0 107 10 US-09-229-200A-15 Sequence 80.0 107 10 US-09-056-160B-15 Sequence 79.4 110 10 US-09-056-160B-103 Sequence 79.4 237 10 US-09-056-160B-100 Sequence 79.3 107 10 US-09-056-160B-102 Sequence 79.1 109 10 US-09-099-102-12 Sequence 79.1 109 10 US-09-099-102-15 Sequence 78.9 107 9 US-09-999-025-15 Sequence 78.9 108 10 US-09-999-025-15 Sequence 78.9 108 10 US-09-999-025-15 Sequence 78.9 109 10 US-09-292-200A-14 Sequence 78.9 109 10 US-09-292-200A-14 Sequence 78.9 109 10 US-09-292-200A-14 Sequence 78.7 108 9 US-10-153-159-2 Sequence 78.7 108 10 US-09-056-160B-8 Sequence 78.7 108 10 US-09-056-160B-8 Sequence 178.7 108 10 US-09-056-160B-9 Sequence |

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Gaps

1;

7; Indels

Query Match 85.3%; Score 479.5; DB 10; Length 108; Best Local Similarity 85.8%; Pred. No. 1e-28; Matches 91; Conservative 7; Mismatches 7; Indels 1;

US-09-229-200A-11

| Sequence 4, p Sequence 107 Sequence 117 Sequence 113 Sequence 2, Sequence 12, Sequence 12, Sequence 12, Sequence 3, Sequence 3, Sequence 6, Sequence 10, Sequence 2, Sequence 10, Sequence 10, Sequence 2, Sequence 10, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 10, Sequence 10, Sequence 2, Sequence 2, Sequence 2, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 2, Sequence 10, Seque | 11 Sequence<br>13 Sequence<br>15 Sequence<br>15 Sequence<br>15 Sequence<br>15 Sequence<br>15 Sequence | binant Antibody<br>Za<br>1.44 Mb STORAGE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
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| US-10-153-159-4<br>US-09-056-160B-11<br>US-09-095-243-73<br>US-09-940-166A-2<br>US-09-940-166A-2<br>US-09-940-166A-1<br>US-09-940-166A-1<br>US-09-956-160B-11<br>US-09-956-087-3<br>US-09-956-087-3<br>US-09-955-087-3<br>US-09-955-087-3<br>US-09-955-087-3<br>US-09-953-794-0<br>US-10-006-771A-2<br>US-10-006-771A-2<br>US-10-006-771A-2<br>US-10-006-771A-2<br>US-10-006-771A-2<br>US-10-006-771A-2<br>US-10-006-771A-2<br>US-10-006-771A-2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | -09-056-160<br>-09-056-160<br>-09-056-160<br>-09-355-925<br>-09-359-053<br>09-797-941A                | 200A  ecific Recombinant Johnson Johnson Plaza Johnson Plaza  8.09/229,200A 999 0wn> III 35,403 ER: ORT-948 ION: 3239 0B                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| US-10-10-10-10-10-10-10-10-10-10-10-10-10-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | NS-09-08-09-08-09-09-09-09-09-09-09-09-09-09-09-09-09-                                                | 9229<br>9229<br>1 1 2 8 1 1 2 2 2 3 2 3 2 3 3 4 3 3 4 3 3 4 3 3 3 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 100 100 100 100 100 100 100 100 100 100                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                       | -200A-11  (a) 1, Application US/09229200  No. US2002009917941  APPLICANT: JO111ffe et al.  TITLE OF INVENTION: CD4 Speci NUMBER OF SEQUENCES: 28  CORRESPONDENCE ADDRESS:  CORRESPONDENCE ADDRESS:  CONTYRY: ONE JOHNSON & JON  STREET: ONE JOHNSON & JON  COUNTRY: USA  COUNTRY: USA  CONFUTER: EADABLE FORM:  MEDIUM TYPE: DISKETTE, 3  COMPUTER: LBM  OPERATION UNMERR: US/O  FILING DATE: 13-Jan-199  CLASSIFICATION DATA:  REGISTRATION NUMBER: 35,  REGISTRATION NUMBER: 35,  REGISTRATION NUMBER: 35,  REGISTRATION NUMBER: 35,  TELECOMMUNICATION INFORMATION:  TELEPHONE: (858) 784-323  MATION FOR SEQ ID NO: 11:  LENGTH: 108  TELEPHONE: (858) 784-323  MATION FOR SEQ ID NO: 11:  LENGTH: 108  TYPE: amino acid  TOPOLOGY: linear  SEQUENCE DESCRIPTION: SEQ ID                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| 7.25                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                       | A-11  AAPDILCATION US/ IS20020099179A1  FORMATION:  CCANT: JO11iffe e  E OF INVENTION:  ER OF SEQUENCES: ESPONDENCE ADDRES  ADDRESSEE: JOHNS  STATE: NJ  CCUNTRY: USA  ZIP: 08933-7003  ZIP: 08933-7003  ZIP: 08933-7003  ZIP: 08933-7003  ZIP: 08933-7003  ZIP: OBERTINE SYSTEM  MEDIUM TYPE: DIS  COMPUTER: IBM  MEDIUM TYPE: DIS  COMPUTER: IBM  MEDIUM TYPE: DIS  ZIP: 08933-7003  ZIP: 08933-7003  ZIP: 08933-7003  ZIP: OBERTING SYSTEM  MEDIUM TYPE: DIS  ZIP: 08933-7003  ZIP: OBERTING SYSTEM  CLASSIFICATION NUMB  REGISTRATION NUMB  REGISTRATION NUMB  REGISTRATION NUMB  REGISTRATION NUMB  REGISTRATION NUMB  REGISTRATION NUMB  LELENGHI: 108  TELERFAX: (968) 5  TELERFAX: (968) 5  TELERFAX: (968) 5  TYPE: AMINO ACID  TOPOLOGY: LINEAR  TYPE: AMINO ACID  T |
| 23 23 23 23 23 23 23 23 23 23 23 23 23 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 227.5<br>227.5<br>225.5<br>25.5<br>5.5                                                                | 2000A<br>11,0<br>11,1<br>11,1<br>11,1<br>11,1<br>11,1<br>11,1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| 01000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | <b>ਰ ਵਾਵਾਵਾਵਾਵਾ</b>                                                                                   | ULT 1<br>09-229<br>equenc<br>atent<br>GENER<br>INFOR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |

CITY: New Brunswick

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Matches
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 1 DIOMIQSPSSLSASVGDRVIITCKASPDINNYLNWYQQTPGKAPKLLIYYTSTLQPGVPS 60
1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Query Match

85.3%; Score 479.5; DB 10; Length 108;
Best Local Similarity 85.8%; Pred. No. 1e-28;
Matches 91; Conservative 7; Mismatches 7; Indels 1;
 APPLICANT: Joiliffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 APPLICANT: Jolliffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
GORRESPONDENCE ADDRESS:
 61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYDNLIFTFGGGTKLQI 106
 61 RFSGSGSCTDYTFTISSLQPEDIATYYCQQYDNLIFTFGQGTKLQI 106
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
 ADDRESSEE: Johnson & Johnson
STREET: One Johnson & Johnson Plaza
 STREET: One Johnson & Johnson Plaza CIIY: New Brunswick
 SOFTWARE: CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
FILING DATE: 13-Jan-1999
CLASSIFICATION: <UNKnown>
 NAME: JOHN W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
TELECOMMUNICATION INFORMATION:
TELEPHONE: (898) 784-3239
TELEFAX: (908) 524-2808
 TOPOLOGY: 11near SEQ ID NO: 15 US-09-229-200A-15
 US-09-229-200A-16; Sequence 16, Application US/09229200A; Patent No. US20020099179A1; GENERAL INFORMATION:
 US-09-229-200A-15; Sequence 15, Application US/09229200A; Patent No. US20020099179A1; GENERAL INFORMATION:
 COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
 ATTORNEY/AGENT INFORMATION:
 INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
 ZIP: 08933-7003
 COUNTRY: USA
 LENGTH:
 RESULT 2
 RESULT 3
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1; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMIQSPSSLSASVGDRVIITCKASPDINNYIAWYQHTPGKAPKLLIHYTSTLQPGVPS 60
 DB 10; Length 108;
 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
 61 RFSGSGSGTDYTFISSLQPEDIATYCLQQYDNLIFTFGGGTKLQI 106
 y Match 83.0%; Score 466.5; DB 10;
Local Similarity 84.9%; Pred. No. 8.8e-28;
hes 90; Conservative 6; Mismatches 9;
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 15, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Presta, Leonard G.
APPLICANT: Devent, Henry B.
APPLICANT: Chem, Yeone M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
 CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/229,200A
FILING DATE: 13-2n-1999
CLASSIFICATION: <URKnown>
ATTORNEY/AGENT INFORMATION:
 NAME: John W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
 SEQUENCE DESCRIPTION: SEQ ID NO: 16
 APPLICATION NUMBER: US/09/056,160B
FILING DAFE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 784-3239
TELEFAX: (908) 524-2808
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
 COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: <Unknown>
 WinPatin (Genentech)
 Genentech, Inc.
 CITY: South San Francisco
STATE: California
COUNTRY: USA
 TYPE: amino acid
 TOPOLOGY: linear
 CURRENT APPLICATION DATA:
 COUNTRY: USA
ZIP: 08933-7003
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
 STREET: 1 DNA Way
 LENGTH: 108
STATE: NJ
 94080
 RESULT 4
US-09-056-160B-15
 US-09-229-200A-16
 SOFTWARE:
 Query Match
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Matches
 Matches
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 1; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Score 446.5; DB 10; Length 110; Pred. No. 2.5e-26;
 DB 10; Length 107;
 8; Mismatches 13; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 61 RFSGSGSGTDYTLTISSLQPEDFATYXCQQYSTVPWTFGQGTKVEIK 107
 Pred. No. 1.5e-26;
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
 80.0%; Score 449.5;
 APPLICANT: Wells, James A.
APPLICANT: Prests, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
APPLICANT: Chen, Yvonne M.
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
 SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION OF ATA
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: HASAK, JANET E.
REGISTRATION NUMBER: 28,616
 Sequence 103, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
 P1093R2
 P1093R2
 OPERATING SYSTEM: PC-DOS/MS-DOS
 REGISTRATION NUMBER: 28,616
REFREENCE/DOCKET NUMBER: P109:
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/255-1896
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
Hasak, Janet E.
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 103:
 REFERENCE/DOCKET NUMBER: P10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
 79.48;
78.58;
 ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
 79.48;
 LENGTH: 107 amino acids TYPE: Amino Acid
 LENGTH: 110 amino acids TYPE: Amino Acid
 85; Conservative
 SEQUENCE CHARACTERISTICS:
 650/952-9881
 Linear
 Best Local Similarity
 Best Local Similarity
 USA
 US-09-056-160B-103
 94080
 US-09-056-160B-103
 TOPOLOGY:
US-09-056-160B-15
 COUNTRY:
 Query Match
 Query Match
 Matches
 RESULT 5
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 Gaps
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 DIOMIQSPSSLSASVGDRVIITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS 60
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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 79.4%; Score 446.5; DB 10; Length 237; 78.5%; Pred. No. 4.6e-26;
9; Mismatches 13; Indels
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 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 61 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGGGTKVEIK 107
 ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
 Sequence 100, Application US/09056160B
Patent No. US200200315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
 Mismatches
 SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
 FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
 ; Sequence 2, Application US/10011125 ; Patent No. US20020142388A1
 28,616
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
 INFORMATION FOR SEQ ID NO: 100: SEQUENCE CHARACTERISTICS:
 Genentech, Inc.
 CITY: South San Francisco
STATE: California
 : 237 amino acids
Amino Acid
 NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:
 84; Conservative
84; Conservative
 650/952-988
 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 1 DNA Way
 Best Local Similarity
 US-09-056-160B-100
 RESULT 6
US-09-056-160B-100
 ADDRESSEE:
 TOPOLOGY:
 COUNTRY:
 TELEFAX:
 US-10-011-125-2
 STREET:
 Query Match
```

```
Sequence 12, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Cowman, Henry B.
APPLICANT: Chen, Yvonne M.
TILLE OF INVENTION: ANTIBODIES
UMMBER OF SEQUENCES: 131
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION WHER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: HSSSK, Janet E.
REGISTRATION NUMBER: 28,616
 P1093R2
 WinPatin (Genentech)
 TELECOMMUNICATION INFORMATION:
 STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
 Query Match 79.3%;
Best Local Similarity 78.5%;
Matches 84; Conservative
 Genentech, Inc
 ; LENGTH: 108 amino acids; TYPE: Amino Acid; TOPOLOGY: Linear US-09-056-160B-12
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 TELEPHONE: 65U/22.
 CORRESPONDENCE ADDRESS:
 COUNTRY: USA
ZIP: 94080
 RESULT 9
US-09-056-160B-12
 ADDRESSEE:
 US-09-056-160B-13
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 1; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Ouery Match 79.4%; Score 446.5; DB 12; Length 491; Best Local Similarity 78.5%; Pred. No. 8.3e-26; Matches 84; Conservative 9; Mismatches 13; Indels 1;
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 E: 3.5 inch, 1.44 Mb floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
 APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta. Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
ITILE OF INVENTION: ANTI-VEGF ANTIBODIES
UNMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
); OTHER INFORMATION: Sequence is synthesized. US-10-011-125-2
 APPLICANT: Chen, Christina Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
 SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION ATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
 P1093R2
 Sequence 13, Application US/09056160B
Patent No. US20020032315A1
 28,616
 REFERENCE/DOCKET NUMBER: P10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
 NFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
 TYPE: PRT
ORGANISM: Artificial Sequence
 Genentech, Inc.
 CITY: South San Francisco
STATE: California
 : 107 amino acids
Amino Acid
 NAME: Hasak, Janet E. REGISTRATION NUMBER:
 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc)
 DNA Way
 OPERATING SYSTEM:
 GENERAL INFORMATION:
GENERAL INFORMATION:
 ADDRESSEE:
 US-09-056-160B-13
 COMPUTER:
 TOPOLOGY:
 LENGTH: 491
 COUNTRY:
 LENGTH:
 STREET:
 SEQ ID NO 2
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 1; Gaps
 1 DIQMIQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Query Match 79.1%; Score 444.5; DB 10; Length 108; Best Local Similarity 78.5%; Pred. No. 3.4e-26; Matches 84; Conservative 11; Mismatches 11; Indels 1;
 DB 10; Length 107;
Score 445.5; DB 10; Length
Pred. No. 2.9e-26;
9; Mismatches 13; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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KESULT 12
US-09-999-040-15
Sequence 15, Application US/09999040
Fublication No. US20020193574A1
GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/999, 040
FILE REPRENCE:
CURRENT APPLICATION NUMBER: US/09/999, 040
PRIOR FILING DATE: 2001-10-31
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1996-10-31
PRIOR FILING DATE: 1996-10-31
NUMBER: WISCOFT WORD APPLICATION NUMBER: US 60/030,173
PRIOR FILING DATE: 1996-10-31
NUMBER: MISCOSOFT WORD 97 SR-2
SEQ ID NO 15
LEWITH: 107
1; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAFPS 60
 1;
 Query Match 78.9%; Score 443.5; DB 9; Length 107; Best Local Similarity 81.1%; Pred. No. 4e-26; Matches 86; Conservative 9; Mismatches 10; Indels 1.
 APPLICANT: Jolliffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
 9; Mismatches 10; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
 STREET: One Johnson & Johnson Plaza CITY: New Brunswick
 ADDRESSEE: Johnson & Johnson
 Sequence 14, Application US/09229200A
; Patent No. US20020099179A1
; GENERAL INFORMATION:
 COMPUTER READABLE FORM:
 86; Conservative
 COUNTRY: USA
ZIP: 08933-7003
 ORGANISM: Homo sapiens
 ; NAME/KEY: REI VL
; LOCATION: 1..107
US-09-999-040-15
 US-09-229-200A-14
 TYPE: PRT
 FEATURE
 Matches
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 APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Harris, William J.
TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/999,025
CURRENT PAPLICATION NUMBER: US/09/999,025
CURRENT PAPLICATION NUMBER: US/09/999,025
PRIOR APPLICATION NUMBER: PCT US97/19641
PRIOR PELING DATE: 1998-02-18
PRIOR FILING DATE: 1998-10-31
PRIOR FILING DATE: 1997-10-30
PRIOR FILING DATE: 1997-10-30
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 33
SUMPRER: Microsoft Word 97 SR-2
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 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
 Query Match 79.1%; Score 444.5; DB 10; Length 109; Best Local Similarity 78.5%; Pred. No. 3.4e-26; Matches 84; Conservative 11; Mismatches 11; Indels 1;
 Score 443.5; DB 9; Length 107; Pred. No. 4e-26;
 APPLICANT: Sharon Erickson
APPLICANT: Sharon Erickson
APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Mark Sliwkowski
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
FILLE REFERENCE: GENERY. 073.2
CURRENT APPLICATION NUMBER: US/09/811,123
CURRENT FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIK 107
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 ; OTHER INFORMATION: Humanized Antibody Sequence US-09-811-123-6
 Sequence 15, Application US/09999025 Publication No. US20020183497A1 GENERAL INFORMATION:
 Sequence 6, Application US/09811123
Patent No. US20020001587A1
GENERAL INFORMATION:
 78.9%;
81.1%;
 ORGANISM: Artificial Sequence
 ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
 ; NAME/KEY: REI VL
; LOCATION: 1..107
US-09-999-025-15
 RESULT 11
US-09-999-025-15
 LENGTH: 107
 -09-811-123-6
 109
 SEQ ID NO 15
 TYPE: PRT
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Gaps

us-09-155-739-7.rapb

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Matches
 RESULT 15
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 Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60
 1;
 Owery Match 78.9%; Score 443.5; DB 10; Length 108; Best Local Similarity 81.1%; Pred. No. 4e-26; Matches 86; Conservative 9; Mismatches 10; Indels 1;
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
FILING DATE: 13-Jan-1999
CLASSIFICATION: <UNKNOWN>
 NAME: JOHN W. Wallen, III
RECISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
TELECOMMUNICATION INFORMATION:
TELEPHONE: (958) 784-3239
TELEFAX: (908) 524-2808
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
 APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
 ; | SEQUENCE DESCRIPTION: SEQ ID NO: 14: US-09-229-200A-14
 SUFTWARENT SPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
 Sequence 105, Application US/09056160B
Patent No. US20020032315Al
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
 REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
 OPERATING SYSTEM: PC-DOS
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAWE: HASAK, JANEL E.
REGISTRATION NUMBER: 28,616
 ATTORNEY/AGENT INFORMATION:
 Genentech, Inc.
DNA Way
 SOFTWARE: <Unknown>
 South San Francisco
California
 TYPE: amino acid
 TOPOLOGY: linear
 CORRESPONDENCE ADDRESS:
 LENGTH: 108
 CLASSIFICATION:
 USA
 US-09-056-160B-105
 94080
 ADDRESSEE:
 STREET: 1
 COUNTRY:
 STATE:
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1; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 2; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 DB 10; Length 110;
 78.8%; Score 443; DB 10; Length 109; 76.9%; Pred. No. 4.4e-26; Live 14; Mismatches 9; Indels
 GENERAL INCORATION:
GENERAL INFORMATION:
APPLICANT: JOILIffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE BODRESS:
ADDRESSEE: Johnson & Johnson
STREET: One Johnson & Johnson
CITY: New Brunswick
 ZIP: 08933-7003
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 Indels
 61 RFSGSGSGRDYSFSISNLEPEDIATYCIQYNDLFLTFGGGTKLEIK 108
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK 106
 13;
 y Match 78.9%; Score 443.5; DB 10
Local Similarity 77.6%; Pred. No. 4.1e-26;
hes 83; Conservative 10; Mismatches 13
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
FILING DATE: 13-Jan-1999
CLASSIFICATION: <u >CLASSIFICATION</u>
 ATTORNEY/AGENT INFORMATION:
NAME: JOHN W. WAllen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
TELECOMMUNICATION INFORMATION:
 TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 (858) 784-3239
 COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: <Unknown>
 Sequence 7, Application US/09229200A Patent No. US20020099179A1
 TELEFAX: (908) 524-2808
INFORMATION FOR SEQ ID NO: 7:
 105:
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 105: SEQUENCE CHARACTERISTICS: LENGTH: 110 amino acids: TYPE: Amino Acid

TOPOLOGY: Linear
US-09-056-160B-105
 SEQUENCE CHARACTERISTICS:
 Query Match /0.00,
Best Local Similarity 76.9%;
Matches 83; Conservative
 TYPE: amino acid
 COUNTRY: USA
 TELEPHONE:
 STATE: NJ
 US-09-229-200A-7
 US-09-229-200A-7
 Query Match
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Search completed: January 6, 2003, 13:29:31 Job time: 5.13939 secs

Page 7

Mon Jan 6 14:19:48 2003

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 6, 2003, 13:12:26; Search time 9.85051 Seconds (without alignments) 1034.490 Million cell updates/sec Run on:

US-09-155-739-7 Title:

562 1 DIQMTQSPSSLSASVGDRVT......YCLQYDNLWTFGQGTKVEIK 106 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched: 283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

S26329
Ig kappa chain V region - mouse
Ig kappa chain S26329
Ig hate: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000
Ig partition S26329
Is xp. Med: 174, 613-624, 1991
Ig partition Antibodies that are specific for a single amino acid interchange in a protein A; Title: Antibodies that are specific for a single amino acid interchange in a protein A; Ascession: S26329
Ig partition S26329
I

A; Molecule type: mRNA A; Residues: 1-104 <STA> A; Cross-references: EMBL:X59173; NID:g52309; PIDN:CAA41883.1; PID:g1334059 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>

DB 2; Length 104;

Score 479;

85.2%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                                                 | 108<br>1129<br>1129<br>1129<br>1139<br>1108<br>1108<br>1117<br>1117                          | 1000000000011100                           | S44122 19 19 19 19 19 19 19 19 19 19 19 19 19                                                                   | kappa C<br>kappa | chain V r<br>chain V r<br>chain pre<br>chain V-I<br>chain V-I<br>chain V-I<br>chain V r<br>chain V r<br>chain V r<br>chain V r<br>chain V r<br>chain V r |          |     |
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                                                                                                                                                                                                                                                                                       |                                                                                                                                 |                                                                                              |                                            | ALIGNMENTS                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                          |          | •   |
| • | RESULT 1 S26330 Ig kappa chain V region - mouse C; Species: Mus musculus (house mouse) C; Date: 13-Jan-1995 #sequence_revision C; Accession: S26330 B. Exp. Med: 174, 613-624, 1991 A; Title: Antibodies that are specific f A, Accession: S26330 A, Accession: S26330 A; Status: preliminary A, Molecule type: mRMA A, Residues: 1-104 <sta> A; Cross-references: EMBL:X59185; NID:95 C; Superfamily: immunoglobulin V regions C; Superfamily: immunoglobulin homology F:16-90/Domain: immunoglobulin homology</sta> | chain<br>13-Jan<br>13-Jan<br>13-Jan<br>13-Jan<br>100: S.E.;<br>Med. 1<br>Amtib<br>Amtib<br>Amtib<br>100: S<br>1: prel<br>1: prel<br>1: prel<br>1: prel<br>2: prel<br>3: prel<br>3: prel<br>3: prel<br>3: prel<br>4: Amtib                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Kappa chain V region Species: Mus musculus Date: 13-Van-1995 #sea Accession: S2630 Stark, S.E., Caton, A Exp. Med. 174, 613-6 Title: Antibodies tha Reference number: S26 Accession: S26330 Status: preliminary Molecule type: MRNA Residues: 1-104 SSTACOSS-references: EMB Superfamily: immunogl Schoolson in immunogl immunogl immunogl immunogl immunogli immunogl | lon -<br>lus (h<br>#seque<br>3-624,<br>that a<br>S26309<br>Y<br>A<br>TAS-<br>TAS-<br>TAS-<br>TAS-<br>TAS-<br>TAS-<br>TAS-<br>TA | mous<br>couse<br>nce_<br>199<br>re s<br>re s<br>re s<br>re s<br>re s<br>re s<br>re s<br>re s | ie mc<br>rev<br>11<br>11D:<br>11D:<br>11D: | n 13-Jan-1995 #text_for a single amino 1421; PMID:1908510 952316; PIDN:CAA4189 pblin hplin y <pre>cMM&gt;</pre> | change 20-Jun-200<br>acid interchange<br>15.1; PID:91334063                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | n-2000<br>hange in                                                                                                                                       | a protei | ij. |
|   | Query M<br>Best Lo<br>Matches                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Ouery Match<br>Best Local S<br>Matches 89                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Ouery Match<br>Best Local Similarity<br>Matches 89; Conser                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | vat                                                                                                                             | 86.8%;<br>85.6%;<br>ive                                                                      | de de                                      | Score 488; DB 2; Length 104<br>Pred. No. 1.6e-35;<br>8; Mismatches 7; Indels                                    | 04;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Gaps                                                                                                                                                     | 0;       |     |
|   | oy<br>Ob                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 1 DION<br>1 -   -   1<br>1 DION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | TTOSPSS.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | LSASVG<br>     : <br> SASLG                                                                                                     | : 1  <br>: 1  <br>:GKVT                                                                      |                                            | DIOMTOSPSSLSASYGDRVTITCKTSQDINKYMAWYOOTPGKAPRLLIHYTSALQPGIPS<br>                                                | SALQPGII<br>        <br>STLQPGIE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 09 Sc<br>11<br>58 60                                                                                                                                     |          |     |
|   | o, da                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 61 RFSG<br>     <br>61 RFSG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | SSGSGRD<br>               <br>  SGSGRD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | YTFTIS<br> : : }<br>YSFSIS                                                                                                      | SLOF<br>:  :  <br>NLEF                                                                       | ED1                                        | RESGSGSGRDYTETISSLOPEDIATYCLQYDNLWTFGQGTKVE 104<br>                                                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          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Local Similarity

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C;Accession: PL0270
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A;Reference number: PL0231; MUID:90111618; PMID:2104919
 PHIO64

Ig light chain V region (clone 202.54) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C;Accession: PHI064

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A;Reference number: PH0971; MUID:92381444; PMID:1512540
 ö
 ij
 Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
 0; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 .;
H
 Length 107;
 A/Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
 A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
 DB 2; Length 97;
 Indels
 Indels
 .
9
 79.4%; Score 446.5; DB 2; 79.4%; Pred. No. 6.4e-32;
 10;
 80.4%; Score 452; DB 2;
85.6%; Pred. No. 2e-32;
tive 8; Mismatches
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTF 97
 97
 11; Mismatches
 F;24-34/Region: complementarity-determining 1 F;35-49/Region: framework 2
 F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
 /Region: complementarity-determining 3
 A; Status: nucleic acid sequence not shown
 Best Local Similarity 85.6
Matches 83; Conservative
 Best Local Similarity 79.49
Matches 85; Conservative
 F;98-107/Region: framework 4
 A; Molecule type: mRNA A; Residues: 1-97 <TIL>
 A; Accession: PH1064
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 Query Match
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 Ig kappa chain V region (VM113) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
R;Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Rroc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A;Reference number: A33936; MUID:89282831; PMID:2471975
 C,Aqcession: S09365
R;Feddersen, R.; van Ness, B.
Nucleic Acids Res. 17, 9787-9809, 1989
A;Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene segm A;Reference number: S09365; MUID:90098844; PMID:2513557
A;Aqcession: S09365
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 C.Species: Mus musculus (house mouse)
C.Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 0; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 0; Gaps
 1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYLAWYQHKPGKGPRLLIHYTSTLQPGIPS 60
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 A; Ctoss-references: GB:J04577; NID:g623187; PIDN:AAA60443.1; PID:g623189
 1;
 DB 2; Length 125;
 ch 85.1%; Score 478; DB 2; Length 106; 1 Similarity 83.0%; Pred. No. 1.2e-34; 88; Conservative 10; Mismatches 8; Indels
 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
 A; Molecule type: DNA
A; Residues: 1-125 <FED>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 33-107/Domain: immunoglobulin homology <IMM>
Pred, No. 9.8e-35;
 10; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW-TFGQGTKVEIK 106
 61 RFSGSGSRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 61 RFSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVE 104
 82.5%; Score 403.2,
83.2%; Pred. No. 2.5e-33;
tive 7; Mismatches 10
 84.6%; Preq.
 Ig kappa chain - mouse (fragment)
 Conservative
 89; Conservative
 Best Local Similarity
Matches 88; Conserv
 Query Match
Best Local Similarity
 A; Molecule type: mRNA
A; Residues: 1-106 <MEE>
 A; Status: preliminary
 A; Status: preliminary
 Query Match
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Matches
 Matches
 78
 RESULT 3
 RESULT 4
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C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #text_change 20-Jun-2000
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a proteil A;Reference number: S26309; MUID:91341421; PMID:1908510
 C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Datession: PL0272
E;Accession: PL0272
J. Exp. Med. 171, 265-297, 1990
A;Title: Auti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A;Reference number: PL0231; MUID:90111618; PMID:2104919
 A;Molecule type: mRNA
A;Residues: 1-103 <27A>
A;Cross-references: EMBL:X59187; NID:952318; PIDN:CAA41897.1; PID:91334064
A;Note: the sequence of residues 1-8 and the corresponding nucleic acid sequence are
 A;Cross-references: EMBL:X59191; NID:g52321; PIDN:CAA41901.1; PID:g1334066 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology

F;16-90/Domain: immunoglobulin homology

IMM>
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS
 Length 103;
 C; Superfamily: immunoglobulin V region; immunoglobulin homology
 10; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 Ig kappa chain V region (anti-DNA, 6B8VK) - mouse (fragment)
 61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKL 103
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKV 103
 DB 2;
 Score 443; DB 2;
Pred. No. 1.2e-31;
 .le-31;
 13; Mismatches
 78.4%; Score 440.5;
78.5%; Pred. No. 2.16
:ive 11; Mismatches
 F;89-97/Region: complementarity-determining 3 F;98-107/Region: framework 4
 F; 24-34/Region: complementarity-determining 1
 78.8%; Score 443; 77.7%; Pred. No. 1
 F;50-56/Region: complementarity-determining F;57-88/Region: framework 3
 C; Keywords: heterotetramer; immunoglobulin
 N; Alternate names: Ig kappa chain V region
 Ig light chain V region - mouse (fragment)
 F;16-90/Domain: immunoglobulin homology
 Ouery Match 78.8%
Best Local Similarity 77.7%
Matches 80; Conservative
 Local Similarity 78.5 es 84; Conservative
 F;35-49/Region: framework 2
 F;1-23/Region: framework
 A;Accession: PL0272
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
 A; Residues: 1-103 <ST2>
 A; Status: preliminary
 A; Molecule type: mRNA
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Matches
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 A; Cross-references: GDB:136264
A; Map position: 2pl2-2pl2
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer
 A Wolecule type: protein
A; Mesiduas: 1-108 cApL;
A; Residuas: 1-108 cApL;
A; Note: the C region of this chain has the Inv (1,2) marker
B; Epp. O.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.
B; Epp. O.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.
B; Epp. O.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.
A; Epp. O.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.
A; Title: The molecular structure of a dimer composed of the variable portions of the Ben
A; Reference number: A90392; MUID: 76039968; PMID: 1182131
C; Comment: annotation; X-ray crystallography, 2.0 angstroms
C; Genetics:
 R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-A;Reference number: S52789
 Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A; Title: Die Primaerstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom vollstaendige Aminosaeuresequenz des Proteins.
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 C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
 C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: AJ1683; AD1873
R;Palm, W.; Hilschmann, N.
 Cross references: EMBL: X85995; NID:9758588; PIDN:CAA59987.1; PID:9758589 Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin
 Gaps
 Gaps
 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 DIQMIQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIHAASSLETGVPS 82
 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIOMTOSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60
 ij
 ij
 Length 129;
 Indels
 Indels
 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 RFSGSGSGRDYTFISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
 Ig kappa chain V-I region (Rei) - human (tentative sequence)
 A; Reference number: A91663; MOID:76023758; PMID:809329
A; Accession: A91663
 10; Mismatches 11;
 DB 1;
 DB 2;
 Score 443.5; DB 1
Pred. No. 1.2e-31;
 78.9%; Score 443.5; DB 279.4%; Pred. No. 1.4e-31;
 9; Mismatches
 38-112/Domain: immunoglobulin homology <IMM>
 F;16-90/Domain: immunoglobulin homology <IMM>F;23-88/Disulfide bonds: #status experimental
 Ig kappa chain V region - human (fragment)
 ch 78.9%;
l Similarity 81.1%;
86; Conservative 9
 79.48;
 Best Local Similarity 79.49
Matches 85; Conservative
 Local Similarity
 A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-129 <ROC>
 A; Accession: S52789
 A; Gene: GDB: IGKV1
 Best Loca
Matches
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Gaps

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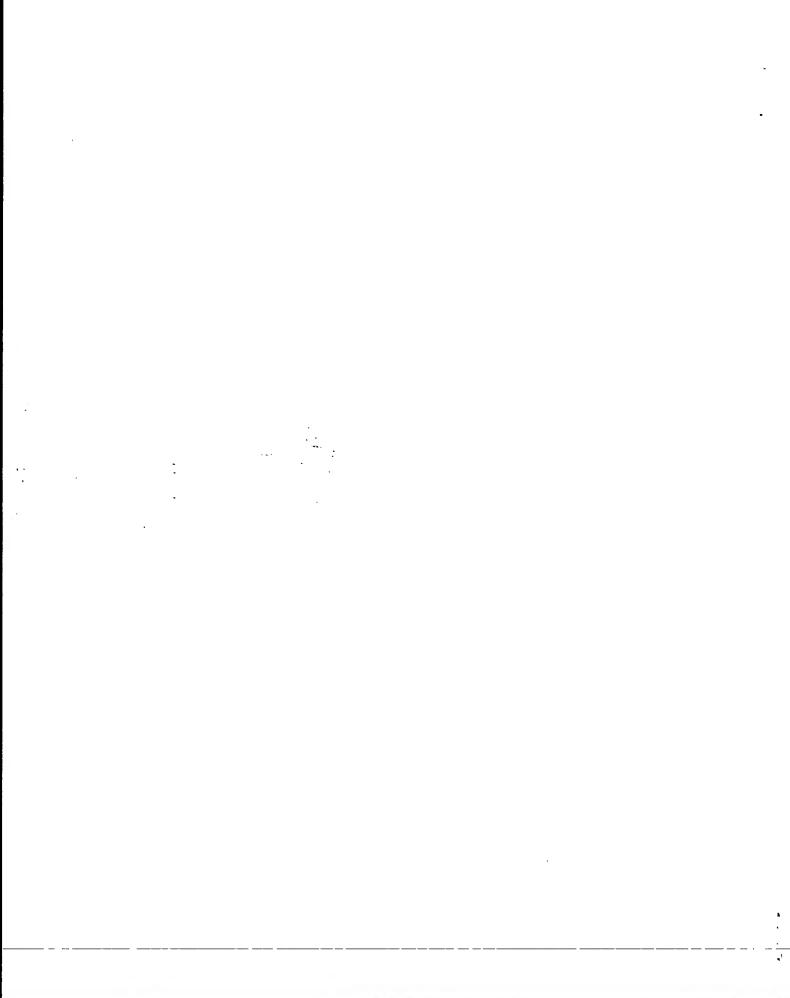
Length 107;

```
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A;Reference number: PLO231; MUID:90111618; PMID:2104919
A;Accession: PLO271
 A; Wolecule type: protein
A; Residues: 1-108 <-SGID
A; Residues: 1-108 <-SGID
A; Residues: 1-108 <-SGID
A; Note: the C region of this chain has the Inv (3) marker
B; Fehlhammer, H; Schliffer, M; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; S
B; Deplys: Struct. Mech. 1, 139-146, 1975
A; Tille: The Structure determination of the variable portion of the Bence-Jones prote
A; Reference number: A90729; MUID:7702243; PMID:1234024
A; Contents: annotation: X-ray crystallography
A; Contents: annotation: X-ray crystallography
A; Contents: annotation of the V region was determined by molecular replacement methods
R; Steiner, V; Chang, J·Y.
FEBS Lett. 222, 6-10, 1987
A; Title: Chemical modification of the carboxyl groups of protein substrates enhances
A; Contents: monotation
 A;Map position: 2p12-2p12 (C:)Complex: an immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds: in some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology (C;Neywords: heterotetramer: immunoglobulin F;16-90/Domain: immunoglobulin homology cIMM> F;23-88/Disulfide bonds: #status predicted
 C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000
C;Dates: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000
C;Accession: A91653; A01862; S02573
R;Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, A;Reference number: A91653; MUID:72189444; PMID:5028201
 ä
 Ig kappa chain V region (anti-DNA, 2F3VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
 1; Gaps
 1 DIOMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALOPGIPS 60
 Length 107;
 A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
 Indels
 12;
 DB 2;
 78.2%; Score 439.5; DB 2
78.5%; Pred. No. 2.6e-31;
Live 10; Mismatches 12
 F;50-56/Region: complementarity-determining 2 F;57-88/Region: framework 3
 F;16-90/Domain: immunoglobulin homology <IMM>F;24-34/Region: complementarity-determining 1
 /Region: complementarity-determining 3
 C; Comment: This is a Bence Jones protein.
 Ig kappa chain V-I region (Au) - human
 Best Local Similarity 78.5% Matches 84; Conservative
 A; Cross-references: GDB:136264
 F;98-107/Region: framework 4
 F;35-49/Region: framework 2
 A; Molecule type: mRNA
 C; Accession: PL0271
 A; Accession: A91653
 A; Gene: GDB: IGKV1
 Query Match
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 Ritawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A; fitle: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A; Reference number: A33730; MUID:89367325; PMID:2505260
A; Accession: E33730
 C.Accession: PLO269
R.Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.; Exp. Med. 171, 265-297, 1990
A.; Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A.Reference number: PLO231; MUID:90111618; PMID:2104919
A.Accession: PLO269
 ;
 Ig kappa chain V region (9.42) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
 C'Species: Mus musculus (house mouse)
C;pate: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
 Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 A; cross-references: GB:MZ6000; NID:9197119; PIDN:AAA38916.1; PID:9197120 CS: Superfamily: immunoglobulin v region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F; 16-90/Domain: immunoglobulin homology <IMM>
 Length 107;
 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
 DB 2; Length 94;
 78.2%; Score 439.5; DB 2; Length 178.5%; Pred. No. 2.6e-31;
Tive 10; Mismatches. 12; Indels
 Score 440; DB 2; Length 94
Pred. No. 2.1e-31;
7; Mismatches 6; Indels
61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107
 19 kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)
 61 RESGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNL 94
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL 94
 F;50-56/Region: complementarity-determining 2 F;57-88/Region: framework 3 F;89-97/Region: complementarity-determining 3
 F:16-90/Domain: immunoglobulin homology <IMM>
 F; 24-34/Region: complementarity-determining 1
 78.3%;
86.2%;
 84; Conservative
 Best Local Similarity 86.2
Matches 81; Conservative
 F;98-107/Region: framework 4
 F;35-49/Region: framework 2
 23/Region: framework
 Local Similarity
 A; Molecule type: mRNA
A; Residues: 1-107 <SHL>
 A; Molecule type: DNA
A; Residues: 1-94 <LAW>
 A; Status: preliminary
 C; Accession: E33730
 Query Match
 Query Match
 Matches
 61
 RESULT 11
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Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C; Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C; Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C; Date: 31-May-1996 #sequence_revision 319154
R; Schormann, N; Murrell, J.R.; Liepnieks, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A; Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposed A; Reference number: 139154
A; Reference number: 139154
A; Mull: 9603804; PMID: 7568160
A; Accession: 139154
A; Accession: 139154
A; Accession: 139154
A; Residues: 1-108 cRES
C; Stoperfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-90/Domain: immunoglobulin homology <IMM>
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 Gaps
 1; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 ij
Length 108;
 DB 2; Length 108;
 Score 435.5; DB 2; Length 1
Pred. No. 5.8e-31;
9; Mismatches 12; Indels
Query Match 78.2%; Score 439.5; DB 1; Length Best Local Similarity 79.4%; Pred. No. 2.6e-31; Matches 85; Conservative 8; Mismatches 13; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIX 106
 61 RFSGSGSGTEYTFTISSLQPEDIATYYCQQYDDLPYFFGGGTKVEIK 107
 Ig kappa chain (BRE) - human (fragment)
 Query Match
Best Local Similarity 79.4%;
Matches 85; Conservative
 RESULT 15
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Search completed: January 6, 2003, 13:18:19
Job time: 9.85051 secs



P01613 homo sapien P01625 homo sapien P04207 homo sapien P04207 homo sapien P01653 mus musculu P01650 mus musculu P01652 mus musculu P01652 homo sapien P01622 homo sapien P01624 homo sapien

KV4A\_HUMAN KV3H\_HUMAN KV3T\_MOUSE KV5T\_MOUSE KV5C\_MOUSE 
1112 1114 1129 1129 1108 1108 1108 1108 1109

63.4 62.0 61.9 61.6 61.5 61.7 60.7 60.7 60.6

356.5 348.5 348.5 348.5 340.45 339.5 339.5 339.5 339.5 339.5

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January 6, 2003, 12:48:25; Search time 5.35354 Seconds (without alignments) 821.231 Million cell updates/sec
 US-09-155-739-7
562
1 DIOMIQSPESSLSASVGDRVT......XCLQYDNLMTFGQGTKVEIK 106
 112892
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 112892 seqs, 41476328 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 SwissProt_40:*
 Title:
Perfect score:
 Scoring table:
 Database :
 Sequence:
 Searched:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|        |       | æ     |                 |    |            |             |       |   |
|--------|-------|-------|-----------------|----|------------|-------------|-------|---|
| Result |       | Query |                 |    |            |             |       |   |
| NO.    | Score | Match | Match Length DB | DB | ID         | Description | tion  |   |
| -      |       | 20 07 | 001             |    |            |             |       |   |
| 1      |       | 0.0   |                 | 4  | NATO TOTAL | /OGTOJ      |       | S |
| 7      | 439.5 | 78.2  |                 | -  | KV1B_HUMAN | P01594      |       |   |
| e      | 421.5 | 75.0  | ,               | ٦  | KV1M HUMAN | P01605      |       |   |
| 4      | 419.5 | 74.6  | .,              | ۳4 | KV1A HUMAN | P01593      |       |   |
| S      | 419.5 | 74.6  | 108             | П  | KV1P HUMAN | P01608      |       |   |
| 9      | 419.5 | 74.6  | -               | -  | KV1Y HUMAN | P80362      | homod |   |
|        |       |       |                 |    |            |             |       |   |

|   |        | Description     | PO1607 homo sapien | homo  | omou o | homo  | Omod 80 | 2 homo     | omod 60    | homod      | homod      | homo  | рошо  | homo  | P04430 homo sapien | P01603 homo sapien | homo       | homo       | homod      | homod      | homo       | homo       |            | homod      | mus m | P01602 homo sapien | P01637 mus musculu | P06313 homo sapien | P01648 mus musculu | P01647 mus musculu | P01612 homo sapien | P01601 homo sapien |            | P01646 mus musculu | P01645 mus musculu |
|---|--------|-----------------|--------------------|-------|--------|-------|---------|------------|------------|------------|------------|-------|-------|-------|--------------------|--------------------|------------|------------|------------|------------|------------|------------|------------|------------|-------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|--------------------|--------------------|
|   |        | ΩI              | KV10_HUMAN         |       | _      | _     |         | KV1Y_HUMAN | KV1Q_HUMAN | KV1W_HUMAN | KV1D_HUMAN |       | KV1   | _     | _                  | KV1K_HUMAN         | KV1E_HUMAN | KV1L_HUMAN | KV1N_HUMAN | KV1C_HUMAN | KV1G_HUMAN | KV1X_HUMAN | KV1S_HUMAN | KV4C_HUMAN | KV5J  |                    |                    |                    | KV5C               |                    |                    | KV1 I_HUMAN        | KV5K_MOUSE | KV5M_MOUSE         | KV5L_MOUSE         |
|   |        | Match Length DB | 108 1              |       |        | 108 1 |         |            | 108 1      | 129 1      | 107 1      |       | 108 1 |       |                    | 108 1              | 108 1      | 108 1      | 108 1      | 108 1      | 108 1      | 129 1      | 108 1      | 134 1      |       | 117 1              |                    | 133 1              |                    |                    |                    | 117 1              | 108 1      | 108 1              | 108 1              |
| p | Query  | Match           | 8                  | 78.2  | ď.     | 74.6  | 4       |            | •          | 72.9       | •          | ٠.    | 71.6  | ٠.    | -                  | 69.5               |            |            |            |            | 68.2       | 68.2       | -:         | 0.79       |       |                    | •                  | ٠.                 | 64.9               | 64.7               | 64.4               | 64.4               | 64.3       | 64.0               | 63.8               |
|   |        | Score           | 443.5              | 439.5 | 421.5  | 419.5 | 419.5   | 419.5      | 413.5      | 409.5      | 409        | 408.5 | 402.5 | 397.5 | 396.5              | 390.5              | 388.5      | 386.5      | 385.5      | 384.5      | 383.5      | 383.5      | 381.5      | 376.5      | 371.5 | 368                | 366.5              |                    | 64                 | 363.5              | 362                | m                  | 61         | 359.5              | 2                  |
|   | Result | . S             | 1                  | 7     | e      | 4     | S       | 9          | 7          | œ          | σ,         | 10    | 11    | 12    | 13                 | 14                 | 15         | 16         | 17         | 18         | 19         | 20         | 21         | 22         | 23    | 24                 | 52                 | 56                 | 27                 | 28                 | 53                 | 30                 | 31         | 32                 | 33                 |

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KV1M_HUMAN
P01605;
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SEQUENCE
 DISULFID
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 KV1M_HUMAN
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 Ϊ;
 Bence-Jones protein Au.";
Biophys. Struct. Mech. 1:139-146(1975).

-i- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF THE KAPPA CHAIN REI.

-i- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-i- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

HISSP; P01607; IREI.
 Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 MEDLINE=72189444; PubMed=5028201;
Schlechl H., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1;
 MEDLINE=77022433; PubMed=1234024;
Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman B.E.,
Schwager P., Steigemann W., Schramm H.J.;
"The structure determination of the variable portion of the
 78.9%; Score 443.5; DB 1; Length 108; ilarity 81.1%; Pred. No. 4.18-40; Conservative 9; Mismatches 10; Indels 1.
 COMPLEMENTARITY-DETERMINING-1.
 FRAMEWORK - 2 .
COMPLEMENTARITY - DETERMINING - 2 .
FRAMEWORK - 3 .
 COMPLEMENTARITY - DETERMINING-3,
52
54
57
61
67
69
75
82
90
98
106
108
A; 11902 MW; 9E8143E1188BCEZA CRC64;
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
 Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972)
 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Imanuoglobulin V region; Bence-Jones protein.
DOMAIN
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
 Ig kappa chain V-I region AU.
 STANDARD;
 X-RAY CRYSTALLOGRAPHY
 85
98
102
108
108 AA;
 Local Similarity
nes 86; Conserv
 NCBI_TaxID=9606;
 protein Au).";
 KV1B_HUMAN
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SEQUENCE
 SEQUENCE.
 Query Match
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 Scand. J. Immunol. 5:677-684(1976).

-1- MISCELLANBOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POW V-II KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDICTYPIC DETERMINANTS.

-1- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

PIR, A01871, KTHULY.

HSSP: P01607; IREI.

InterPro; IPR003596; Ig_MHC.
 1; Gaps
 3; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIOMIQSPSSLSVSVGDRVIIICQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS 60
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Capra J.D., Klapper D.G.; Complete amino acid sequence of the variable domains of two human IgM anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 DB 1; Length 108;
 Length 108;
 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
 FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
 FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK 106
 Indels
 Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 61 RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIK 107
98 107 FRAMEWORK-4.
23 88 BY SIMILARITY.
108 108 Ap. 11939 MW; E8011187EEEFFFF99 CRC64;
 11834 MW; 739993A95431434A CRC64;
 75.0%; Score 421.5; DB 1; 75.0%; Pred. No. 8.7e-38;
 Query Match 78.2%; Score 439.5; DB 1; Best Local Similarity 79.4%; Pred. No. 1.1e-39; Matches 85; Conservative 8; Mismatches 13;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Aappa chain V-I region Lay.
Homo sapiens (Human).
 BY SIMILARITY.
 11; Mismatches
 FRAMEWORK-4
 MEDLINE=77038198; PubMed=824717;
 81; Conservative
 STANDARD;
 Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region.
 57
89
98 1
23
108 1
 Query Match
Best Local Similarity
 NCBI_TaxID=9606;
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InterPro; IPR003596; Ig_v.
 108 AA;
 Local Similarity
 KV1Y_HUMAN
P80362;
 DISULFID
NON_TER
SEQUENCE
 Query Match
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 Matches
 KV1Y_HUMAN
 19
a
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 qq
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 1;
 Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:5550(1599).
-I. MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 Gaps
 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINHYLNWYQQGPKRAPKILIYDASNLETGVPS 60
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.).";
 1;
 74.6%; Score 419.5; DB 1; Length 108;
 COMPLEMENTARITY - DETERMINING - 1.
 COMPLEMENTARITY-DETERMINING-2.
 FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
 15; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 11992 MW; E3B3B246C18F0C4F CRC64;
 Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
[2]
 Pred. No. 1.4e-37;
9; Mismatches 15
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
119 kappa chain V-I region Roy.
Homo sapiens (Human).
 Bence-Jones protein.
 108 AA.
 108 AA
 FRAMEWORK - 4.
 FRAMEWORK - 1
 FRAMEWORK - 7
 PRT;
 PRT;
 MEDLINE-69234734; PubMed-4893682;
 MEDLINE-68362076; PubMed-5595110;
 Ig kappa chain V-I region AG.
 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
 76.68;
 Pfam; PF00047; ig; 1. SMART; SMO0406; IGv; 1. Immunoglobulin V region;
 Conservative
 STANDARD;
 STANDARD;
 Homo sapiens (Human).
 PIR; A01861; K1HUAG.
HSSP; P01607; 1REI.
 108 AA;
 Similarity
 Hilschmann N.;
 KV1A_HUMAN
P01593;
 KV1P_HUMAN
P01608;
 NON_TER
SEQUENCE
 SEQUENCE
 DISULFID
 Query Match
 SEQUENCE
 Local
 DOMAIN
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 KV1A_HUMAN
 KV1P_HUMAN
 Matches
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1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Gaps
 REVISIONS TO 39 AND 41.
Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;
(In) Franck F., Shugar D. (eds.);
Gamma globulins: structure and function, pp.57-74, Academic Press,
 structural origin of altered domain interactions in immunoglobulin light-chain dimers.";
 Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M., Popp R.A., Solomon A.;
"Characterization and preliminary crystallographic data on the VL-related fragment of the human kI Bence Jones protein Wat.";
J. Mol. Biol. 147:185-193(1981).
 Ig kappa chain V-I region WAT.

Homo sapiens (Human).

Busaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Hudang D. B., Chang C. H. Ainsworth C., Bruenger A.T., Eulitz M., Solomon A., Stevens F.J., Schiffer M.; "Comparison of crystal structures of two homologous proteins:
 New York (1969).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 1;
 DB 1; Length 108;
 COMPLEMENTARITY-DETERMINING-1.
 FRAMEWORK - 3.
COMPLEMENTARITY - DETERMINING - 3.
 COMPLEMENTARITY - DETERMINING - 2.
 13; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 11782 MW; F5ACEDE5A313DF3A CRC64;
 SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 MARKER.

1- MISCELLANEDUS: THIS IS A BENCE-JONES PROTEIN.
PIS, A01874; RIHURY.
HSSP, P603362; IWTL.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003506; Ig_W.
Pfam; P700047; ig; 1.
SWART; SW00406; IGv; 1.
Immunoglobulin V region; Bence-Jones protein.
 ; Score 419.5; DB ; Pred. No. 1.4e-37; 12; Mismatches 1:
 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
 BY SIMILARITY.
 108
 FRAMEWORK-1
 FRAMEWORK - 2
 FRAMEWORK - 4
 PRT;
 Biochemistry 33:14848-14857(1994).
 SEQUENCE OF 1-35,
MEDLINE-81267384; PubMed-6167731;
 MEDLINE=95086080; PubMed=7993911;
 74.68;
75.78;
 PDB; 1WTL; 01-NOV-94.
InterPro; IPR003006; Ig_MHC.
 81; Conservative
 STANDARD;
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 23 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVTS 82
 1 DIOMIQSPSSLSASVGDRVIITCQASQDIRKHLNWYDQRPGRAPRLLIYGASTLETGVPS 60
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
1 DIQMIQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 MEDLINE-85014148; PubMed-6091049; Klobeck H.G., Combriato G., Zachau H.G.; Immunoglobulin genes of the Kappa light chain type from two human lymphoid cell lines are closely related."; Nucleic Acids Res. 12:6995-7006(1984).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 IG KAPPA CHAIN V-I REGION WALKER.
 DB 1; Length 129;
 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
 COMPLEMENTARITY - DETERMINING-2.
 COMPLEMENTARITY-DETERMINING-3.
 16; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
 61 RFSGSGSGTDFTLTISTLQPEDIGNYCQQYDNVPITFGQGTRVENK 107
 RESGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 14069 MW; F941FA07D4AFC2F9 CRC64;
 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Walker precursor.
 72.9%; Score 409.5; DB
74.8%; Pred. No. 2e-36;
iive 10; Mismatches
 BY SIMILARITY.
 FRAMEWORK-4
 FRAMEWORK-2
 FRAMEWORK-3
 EMBL; X00965; CAA25477.1; ALT_TERM.
PIR; A01883; K1HUWK.
 Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
 HSSP, P01607; IREI.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
 Local Similarity 74.89 les 80; Conservative
 STANDARD;
 Homo sapiens (Human).
 45
129
129 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 KV1W_HUMAN
P04431;
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 Query Match
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 KV1D_HUMAN
 KV1W_HUMAN
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 61
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 Eulitz M., Hilschmann N.;
"The primary structure of a human immunoglobulin L-chain of
kappa-type (Bence-Jones protein Scw.), II: The chymotryptic peptides
and the complete amino acid sequence.";
Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 Gaps
 1; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
 1;
 73.6%; Score 413.5; DB 1; Length 108; 74.8%; Pred. No. 6.1e-37; ive 10; Mismatches 16; Indels 1
 Score 419.5; DB 1; Length 108; Pred. No. 1.4e-37;
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FRAMEWORN - 1.
COMPLEMENTARITY - DETERMINING - 1.
 COMPLEMENTARITY - DETERMINING - 2.
 COMPLEMENTARITY-DETERMINING-1.
 COMPLEMENTARITY - DETERMINING-2.
 COMPLEMENTARITY-DETERMINING-3.
 COMPLEMENTARITY-DETERMINING-3
 11; Mismatches 14; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 61 RFSGSGSGTDFTFTISSLQPEDIATYCQQYDTLPLFFGGGTKVDIK 107
 11764 MW; 32CECDDDF964414 CRC64;
 11737 MW; D9D941B3F0FAE697 CRC64;
 BY SIMILARITY.
TN -> SD (IN REF. 2).

 -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region Scw.
 V region; Bence-Jones protein.
 BY SIMILARITY.
 FRAMEWORK-4.
 FRAMEWORK-2
 FRAMEWORK-1
 FRAMEWORK - 3
 FRAMEWORK-3
 FRAMEWORK-1
 MEDLINE=75059271; PubMed=4435756;
 74.6%;
 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SWART; SM00406; IGV; 1.
 81; Conservative
 80; Conservative
 STANDARD;
 PIR; A01875; K1HUSW.
HSSP; P01607; 1REI.
 Homo sapiens (Human).
 Query Match
Best Local Similarity
 108 AA;
 108 AA;
 Query Match
Best Local Similarity
 Immunoglobulin
 KV10_HUMAN
P01609;
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Matches
 KV1H_HUMAN
 Matches
 RESULT 11
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 Goni F., Frangione B.;
"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3.4-pyruvylated
galactose in Klebsiella polysaccharides Klo3,";
Proc. Natl. Acad. Sci. U.S., 80:4837-4841(1983).
--- MISCELLANBOUS: FHIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 1 DIQMIQSPSTLSASVGDRVAITCRASQNISSWLAWYQQKPGKAPKVLIYKSSSLESGVPS 60
 0; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 -1- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN. PROSECTION. PROSECTION. PROSECTION. PROSECTION. PROSECTION. PROSECTION. INTL. INTERPRETATION. IPRO03596; Ig_MHC.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID-9606;
 Eur. J. Biochem. 49:377-391(1974).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 Milstein C.P., Deverson E.V.;
"Primary structure of kappa light chain from a human myeloma
 Length 107;
 13; Indels
 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;
 / Match 72.8%; Score 409; DB 1; Local Similarity 68.9%; Pred. No. 1.8e-36; hes 73; Conservative 20; Mismatches 13.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region CAR.
 P01610;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region WEA.
 107 AA
 108 AA
 WALDENSTROM'S MACROGLOBULINEMIA.
PIR; A01876; K1HUWE.
 PRT;
 MEDLINE=75075135; PubMed=4216454;
 MEDLINE-83273707; PubMed-6410398;
 HSSP; P80362; IWTL.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_v.
Pfam: PF00047; Ig; I.
SMART; SM00406; IGv; I.
 STANDARD;
 STANDARD;
 Homo sapiens (Human)
KV1D_HUMAN
P01596;
 KV1R_HUMAN
 SEQUENCE
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 Query Match
 protein.
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 KV1R_HUMAN
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Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).

-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

-IN THIS A01868; KINHUH.

HSSP; P80362; IWTL.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003006; Ig_W.

Fram; PR0047; ig; 1.

SMART; SM00406; IGv; 1.
 Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Gaps
 DIOMIOSPSSLSASVGDRVIITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Watanabe S., Hilschmann N.; "The primary structure of a monoclonal kappa-type immunoglobulin Lichain of subgroup I (Bence-Jones Protein Hau): subdivision within
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1;
 72.7%; Score 408.5; DB 1; Length 108; 72.0%; Pred. No. 2e-36;
 71.6%; Score 402.5; DB 1; Length 108; 72.9%; Pred. No. 8.8e-36; Live 12; Mismatches 16; Indels 1.
 COMPLEMENTARITY - DETERMINING - 1.
 COMPLEMENTARITY - DETERMINING - 2.
 COMPLEMENTARITY - DETERMINING - 3.
 COMPLEMENTARITY - DETERMINING - 1.
 COMPLEMENTARITY - DETERMINING - 2
 COMPLEMENTARITY - DETERMINING - 3
 17; Indels
 11840 MW; 9249B61F0945618C CRC64;
 11671 MW; 08D3A6160D8D0618 CRC64;
 21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Hau.
V region; Monoclonal antibody.
 Immunoglobulin V region; Bence-Jones protein.
 12; Mismatches
 BY SIMILARITY.
 BY SIMILARITY.
 FRAMEWORK - 3.
 FRAMEWORK - 4
 FRAMEWORK - 2
 FRAMEWORK - 2
 FRAMEWORK - 3
 FRAMEWORK-4
 FRAMEWORK-1
 MEDLINE=71032830; Pubmed-4097974;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
15-JUL-1999 (Rel. 38, Last anno
 77; Conservative
 Conservative
 STANDARD;
 23
34
49
56
88
107
108
 Homo sapiens (Human).
 108 AA;
 108 AA;
 Local Similarity
 Query Match
Best Local Similarity
 NCBI_TaxID=9606;
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"Comparative structural studies on the light chains of human immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker."; J. Biochem. 77:1277-1296(1975).

- HISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-I region Ka.
17 kappa chain V-I region Ka.
18 kappa chain V-I region Ka.
19 kappa chain V-I region Ka.
19 kappa chain V-I region Ka.
19 kappa chain V-I region Ka.
10 kappa chain V-I region Ka.
11 kappa chain V-I region Ka.
12 kappa chain V-I region Ka.
11 kappa chain V-I region Ka.
12 kappa chain V-I region Ka.
13 kappa chain V-I region Ka.
14 kappa chain V-I region Ka.
15 kappa chain V-I region Ka.
16 kappa chain V-I region Ka.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
 MEDLINE=86174817; PubMed=3083240;
MEDLINE=86174817; PubMed=3083240;
Multer F.E., O'Connor T.P., Benson M.D.;
Polymcraphism in a kappa I primary (AL) amyloid protein (BAN).";
Mol. Immunol. 23:73-78(1986).
PIR; A01878; KIHUBN.
PIRSP; PR030362; HTML.
InterPro; IPR03006; Ig_MHC.
InterPro; IPR03596; Ig_V.
 1;
 DB 1; Length 108;
 FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
 COMPLEMENTARITY-DETERMINING-1.
FRAMEMORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEMORK-3.
 COMPLEMENTARITY - DETERMINING - 1.
 COMPLEMENTARITY-DETERMINING-3.
 Indels
 61 NFTGSGSGTDFILTISSLQPEDFATYYCQQYNSYPYTFGQGTKVQIK 107
 CD3FD944FE96FD37 CRC64;
 70.6%; Score 396.5; DB 1; 70.1%; Pred. No. 3.8e-35; ive 14; Mismatches 17;
 PIR; A01869; KIHUKA.

HSSP; P801562; IWTL.

InterPro; IPR003006; Ig_MHC.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGy, 1.

DOMAIN 1 23 FRAMEWORK-1.
 PRT; 108 AA.
 BY SIMILARITY.
 FRAMEWORK-1.
 FRAMEWORK - 3.
 FRAMEWORK-4
 Immunoglobulin V region; Amyloid.
DOMAIN
 MEDLINE=76189985; PubMed-818073;
 11840 MW;
 Local Similarity 70.1% nes 75; Conservative
 STANDARD;
 Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
 56
88
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 108 AA;
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 NCBI_TaxID=9606;
 Shinoda T.;
 KV1K_HUMAN
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 1;
 Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain."; Biochemistry 9:3155-3161(1970).
 1; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1998 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region EU.
19 kappa chain V-I region EU.
20 kappa chain V-I region EU.
21 kappa chain V-I region EU.
22 kappa chain V-I region EU.
23 kappa chain V-I region EU.
24 kappa chain V-I region Eu.
25 kappa chain V-I region EU.
26 kappa chain V-I region EU.
26 kappa chain V-I region EU.
27 kappa chain Eu.
28 kappa chain EU.
 ; Score 397.5; DB 1; Length 108;
; Pred. No. 3e-35;
16; Mismatches 15; Indels 1.
 COMPLEMENTARITY - DETERMINING-1.
 COMPLEMENTARITY - DETERMINING - 2.
 FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQNYITPTSFGQGTRVEIK 107
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYD-NLWTFGQGTKVEIK 106
 11788 MW; 9CD294F2F4D88823 CRC64;
 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-I region BAN.
Homo sapiens (Human).
 1.08 AA
 108 AA
 FRAMEWORK-1
 FRAMEWORK-4
 FRAMEWORK-2
 PRT;
 PRT;
 DISULFIDE BOND.
MEDLINE=71064027; PubMed=4923144;
 MEDLINE=71064023; PubMed=5489770;
 70.7%;
70.1%;
 75; Conservative
 STANDARD;
 STANDARD;
 108 AA;
 Similarity
 NCBI_TaxID=9606;
 KV1V_HUMAN
P04430;
 KV1F_HUMAN
P01598;
 SEQUENCE.
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KV1V_HUMAN
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 HUMAN
 61
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 MEDIANG-72053133; PubMed=5124396;
Milstein C.P., Deverson E.V.;
Milstein C.P., Deverson E.V.;
"The amino acids Sequence of a human kappa light chain.";
Biochem. J. 123:945-958(1971).
-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
HSSP; PO1607; IREI.
INTERPO: IRRO3396; Ig_MHC.
InterPro: IRR03396; Ig_V.
InterPro: IRR03396; Ig_V.
SMART; SMO406; IG; 1.
 Gaps
 1 DIOMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Gaps
 Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 69.1%; Score 388.5; DB 1; Length 108; ilarity 68.9%; Pred. No. 2.6e-34; Conservative 13; Mismatches 19; Indels 1.
 DB 1; Length 108;
 COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
BY SIMILARITY.
 COMPLEMENTARITY - DETERMINING-1.
 COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
 COMPLEMENTARITY - DETERMINING - 2.
97 CCM. FRAMEWORK-4.
107 FRAMEWORK-4.
88 BY SIMILARITY.
108
A, 11900 MW; 768839FBED5A2F4B CRC64;
 69.5%; Score 390.5; DB 1; Length 66.4%; Pred. No. 1.6e-34; Live 19; Mismatches 16; Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
|||| ||| ::||||||::|
61 RFSGQGSGTBFTFTISSV2PZBFATYYCQZYLDLPRTFGQGTKVDLK 107
 FRAMEWORK-1.

COMPLEMENTARITY-DETERMINING-FRAMEWORK-2.

COMPLEMENTARITY-DETERMINING-BERAMEWORK-3.

COMPLEMENTARITY-DETERMINING-FRAMEWORK-3.

COMPLEMENTARITY-DETERMINING-BERAMEWORK-4.

BERAMEWORK-1.

107

FRAMEWORK-1.

108

BY SIMILARITY.

11661 MW; BDD6E350017F1E51 CRC64;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region DEE.
 108 AA.
 PRT;
 Local Similarity 66.4%
les 71; Conservative
 STANDARD;
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Search completed: January 6, 2003, 13:15:47 Job time : 6.35354 secs

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23
 ; Search time 19.9152 Seconds (without alignments) 1096.702 Million cell updates/sec
 562
1 DIOMIQSPSSLSASVGDRVT......YCLQYDNLWTFGQGTKVEIK 106
 671580
 GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 671580 seqs, 206047115 residues
 6, 2003, 13:10:51;
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_human:*
5: Sp_nammal:*
5: Sp_mammal:*
5: Sp_nammal:*
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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 Perfect score:
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 Database :
 Sequence:
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 Run on:
 Title:
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## Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_vertebrate:\*
sp\_unclassified:\*

sp\_rvirus:\*
sp\_bacteriap:\*

sp\_archeap:\*

sp\_organelle:\*
sp\_phage:\*
sp\_plant:\*
sp\_rodent:\*

10:

SUMMARIES

| Result |       | &<br>Query |                 |    |        |                     |
|--------|-------|------------|-----------------|----|--------|---------------------|
| No.    | Score | Match      | Match Length DB | DB | ΩI     | Description         |
| -      | 428.5 | 76.2       | 108             | 4  | Q9UL77 | 09ul77 homo sapien  |
| ~      | 418   | 74.4       | 241             | 11 | Q921A6 | 0921a6 mus musculu  |
| m      | 414   | 73.7       | 107             | 4  | 096SA9 | Ogesa9 homo sapien  |
| 4      | 406.5 | 72.3       | 108             | 4  | Q9UL70 | Ogul70 homo sapien  |
| S      | 395   | 70.3       | 107             | 4  | Q9UL81 | Ogul81 homo sapien  |
| ø      | 385.5 | 68.6       | .108            | 4  | 09UL79 | Ogul79 homo sapien  |
| ۲.     | 384.5 | 68.4       | 214             | 11 | Q9R1A5 | O9r1a5 mus musculu  |
| œ      | 379.5 | 67.5       | 233             | 11 | 091WS9 | O91ws misculus      |
| 6      | 369.5 | 65.7       | 234             | 11 | OBR062 | OBro62 mis misculu  |
| 10     | 365.5 | 65.0       | 116             | 4  | Q96PF6 | Ogeofe homo sapien  |
| 11     | 362.5 | 64.5       | 107             | 11 | 09JL84 | 091184 mis miscol   |
| 12     | 355.5 | 63.3       | 234             | Π  | O91WF8 | 091wf8 mis misculu  |
| 13     | 353.5 | 62.9       | 109             | 11 | O920E6 | O920ee mus musculu  |
| 14     | 337.5 | 60.1       | 298             | 1  | OSOXFO | Ogavfo mis miscular |
| 15     | 336.5 | 59.9       | 108             | 4  | Q9UL83 | Ogul83 homo sapien  |
| 16     | 335.5 | ,59.7      | 234             | 11 | 08VCP0 | O8vco mus musculu   |

| Q9u186 homo sapien Q9u186 homo sapien Q9u186 homo sapien Q9u186 homo sapien Q9u186 mus musculu Q8v100 mus musculu Q9u100 mus musculu Q8tcd homo sapien Q8vci6 mus musculu Q8vci6 mos sapien Q8uvk homo sapien Q8uvk homo sapien Q9u182 homo sapien Q9u182 homo sapien | MENTS     | 108 A puence ortation chain chain ta; Ve. hini; labian leamat.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | rd .                                           | YLNWYQQKPGKAPNLLIYAASSLQSGVPS 60 |
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| 09UL85<br>09UL78<br>09UL78<br>09L559<br>08V170<br>09ER29<br>0920E9<br>09174<br>091174<br>099M37<br>099M37<br>099M37<br>099M37<br>099M37<br>099H2<br>099H2<br>099H2<br>097L8<br>08VC5<br>097L82<br>08VC5<br>097L82<br>08VC16<br>097L82<br>097L82                                                                                                                                                                                                                                                                                                                                                                                                                   | ALIGNMENT | er mixiging DO K - 80 L                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Score 4 Pred. N 8; Mism KTSQDINK               | RASQSISS                         |
| 444111111111111111111111111111111111111                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |           | 13, 13, 19, 19, 19, 19, 19, 19, 19, 19, 19, 19                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | .2%;<br>.6%;<br>e<br>VTITC                     | TITC                             |
| 1009<br>1009<br>1009<br>1009<br>1009<br>1009<br>1009<br>1009                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |           | PRELIMINARY;  (TrEMBLrel. 13, (TrEMBLrel. 13, 10 inmunoglobul (Human).  (139; PubMed-961.  (139; PubMed-961.  (137; Amb56273.1);  (1181.  (1181.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108.  (108 | 76.<br>y 76.<br>rvative<br>ASVGDRV             | ASVGDRV                          |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |           | PRELIMIN, 000 (TrEMBLr, 001 (TrEMBL, 001 | h<br>Similarity<br>82; Conserv<br>QMTQSPSSLSAS | SPSSLS                           |
| 17<br>18<br>18<br>19<br>20<br>21<br>22<br>23<br>23<br>23<br>23<br>23<br>23<br>24<br>30<br>25<br>30<br>26<br>30<br>27<br>30<br>28<br>30<br>29<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20                                                                                                                                                                                                                                                                                                                                                                                                                                                          |           | 10UL77  UUL77;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Na O                                           | 1 DIOMTO                         |
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
 Query Match
Best Local Similarity 72.9%
 PRELIMINARY;
 PRELIMINARY;
 Homo sapiens (Human).
 NON_TER 108 1 SEQUENCE 108 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 NCBI_TaxID=9606;
 (Fragment).
 (Fragment)
 Young D.C
 fetus.";
 Q9UL81
Q9UL81;
 Q9UL70
 RESULT 5
 RESULT 4
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 MEDLINE-98170165; PubMed-9509426;
MEDLINE-98170165; PubMed-9509426;
Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
"Cloning and characterization of cDNAs encoding VH and VL of a monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and generation of a single-chin FV molecule (sCFV).";
Mol. Cells 7:816-819(1997).
EMBL; U88067; AAB48044.1;
InterPro: IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
NON_TER
 Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
 ;
0
 74.4%; Score 418; DB 11; Length 241; 73.6%; Pred. No. 2.2e-39; tive 12; Mismatches 16; Indels (
61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
 61 RFSGSGSGTDFTLTISSLOPEDFATYYCQQSYSTSWTFGEGTKVEIK 107
 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
 241 241 241 26086 MW; 0276887248E9C771 CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DHAR-2002 (TrEMBLrel. 20, Last annotation update)
Anti-CBA 79 single chain Fv fragment (Fragment).
Mus musculus (Mouse).
 107 AA.
 PRT;
 PRT;
 variable region (Fragment).
 78; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Pfam; PF00047; ig; 1.
 Homo sapiens (Human)
 Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 107
 NON_TER
SEQUENCE
 SEQUENCE
 Query Match
 NON TER
 Q96SA9;
 096SA9
 0921A6
 Matches
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Q96SA9
 RESULT 2
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 1 DIOMIQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKRGKAPKLLIYAASSLQSGVPS 60
 1; Gaps
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 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 'Myosin-reactive autoantibodies in rheumatic carditis and normal
 ö
 Length 108;
 Length 107;
 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 01-MAY-2000 (TIEMBLrel. 13, Created)
U-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-DEC-2001 (TIEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
 17; Indels
 Indels
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCOKYNSAPRTFGPGTKLEIK 107
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 11633 MW; B7BEDC3E41FCCA37 CRC64;
 72.3%; Score 406.5; DB 4; 72.9%; Pred. No. 1.7e-38; tive 12; Mismatches 16;
% Ouery Match 73.7%; Score 414; DB 4; Best Local Similarity 75.5%; Pred. No. 2.4e-39; Matches 80; Conservative 9; Mismatches 17;
 Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035044; AAD56280.1; -.
HSSP; P01607; IRRI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR005596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
 108 AA.
 SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
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107 AA.

PRT;

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 Gaps
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 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 Myosin-reactive autoantibodies in rheumatic carditis and normal
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 1;
 Score 385.5; DB 4; Length 108;
Pred. No. 4.1e-36;
8; Mismatches 21; Indels 1
 SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 70.3%; Score 395; DB 4; Length 107; 71.7%; Pred. No. 3.4e-37; Live 10; Mismatches 20; Indels
 01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
 RFSGSGGRDYTFTISSLQPEDIATYCLQYDNL-WTFGGGTKVEIK 106
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
 61 RFSGSGSGTDFTLTISGLQAEDFATYYCQQSYSALTFGPGTKVDIR 106
 108
11787 MW; DB5845F19724FB4E CRC64;
 107 AA; 11501 MW; 070549FDE0754748 CRC64;
 Ciin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035035; AAD56271.1; --.
HSSP, P01607; IREI.
InterPro: IPR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
 Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AR035033, AAD56269.1; -
EMBL, PO16607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
FF00047; ig; 1.
SMART; SM00406; IGV; 1.
MEDLINE=98277139; PubMed=9614934;
 68.68;
72.08;
 Best_Local Similarity 71.7%
Matches 76; Conservative
 Local Similarity 72.0 tes 77; Conservative
 PRELIMINARY;
 107
 108 AA;
 Wu X., Liu
Young D.C.;
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 Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Amb 7, its light and heavy chains) and construction of a single chain antibody (scFV)...;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF153371; AAD40242.1;
HISSP; D01679; ZFBJ.
InterPro; IPR003606; Ig_AHC.
InterPro; IPR003596; Ig_MC.
 1 DIQLIQSPSSMYASLGERVIITCKASQDINSYLSWFQQKPGKSPKILIYRANRLVDGVPS 60
 Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Gaps
 01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TREMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Kappa light chain of Mab7 (Fragment).
Kappa light chain of Mab7 (Fragment).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 1;
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 DB 11; Length 214;
 67.5%; Score 379.5; DB 11; Length 233; 69.2%; Pred. No. 5e-35; Live 12; Mismatches 20; Indels 1;
 Query Match 68.4%; Score 384.5; DB 11; Length Best Local Similarity 66.4%; Pred. No. 1.2e-35; Matches 71; Conservative 18; Mismatches 17; Indels
 Strausberg R;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC013496, AMH13496.1;
InterPro: IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
 SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.8 kDa protein (Fragment).
 214 AA
 Pfam; PF00047; ig; 2.
SMART; SMO406; igy; 1.
SMART; SMO0410; iG_like; 1.
PROSITE; PS00290; iG_MHC; UNKNOWN_1.
 74; Conservative
 PRELIMINARY;
 PRELIMINARY;
 214
 Hypothetical protein
 Best Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID-10090;
 TISSUE-COLON;
 NON_TER
SEQUENCE
 Query Match
 Q9R1A5
Q9R1A5;
 NON_TER
 Q91WS9
Q91WS9;
 NON TER
 Matches
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 RESULT 8
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1 Similarity 66.4%; Pred. No. 8.4e-34; 71; Conservative 14; Mismatches 21; Indels
 PRT; 107 AA
 234 AA.
 PRT;
 PRELIMINARY;
 PRELIMINARY;
 Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
 107
 Mus musculus (Mouse).
Best Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID-10090;
 107
 Strausberg R.;
 TISSUE=COLON;
 (Fragment).
 NON_TER
NON_TER
SEQUENCE
 Q9JL84;
 Q91WF8;
 09JL84
 Q91WF8
 RESULT 11
Q9JL84
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 20 DIQMIQITSSLSASLGDRVIISCSGSGGGIANYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 79
 1; Gaps
 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Hypothetical 25.9 kba protein.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
 MEDLINE-21361171; PubMed-11468171; Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.; The tropism of organ involvement in primary systemic amyloidosis: contributions of Ig V(L) germ line gene use and clonal plasma cell
 Homo sapiens (Human),
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 65.7%; Score 369.5; DB 11; Length 234; 66.4%; Pred. No. 6.9e-34; Ive 14; Mismatches 21; Indels 1;
 Score 365.5; DB 4; Length 116;
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC027418; AAH27418.1; -. Hypothetical protein.
 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;
 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Kappa 1 light chain variable region (Fragment).
SDNK1.
 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 116 AA.
 234 AA
 PRT;
 PRT;
 Blood 98:714-720(2001).
EMBL; AF361758; AAK51465.1; -.
InterPro; IPR003006; Ig_MHC.
 65.08;
 71; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Pfam; PF00047; ig; 1.
 Query Match
Best Local Similarity
Matches 71; Conserv
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 TISSUE=COLON;
 SEQUENCE
 SEQUENCE
 Query Match
 NON_TER
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 Q96PF6;
 08R062
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Q96PF6
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1; Gaps
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1; Gaps
 9
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS
 DB 11; Length 107;
 Query Match 64.5%; Score 362.5; DB 11; Length Best Local Similarity 65.4%; Pred. No. 1.7e-33; Matches 70; Conservative 11; Mismatches 25; Indels
 61 RFSGSGSGXDYSLTISNLEPEDIATYYCQQYSKFPWTFGGGTKLEIK 107
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 61 RFSGGGSAINFIVIISSLQPEDFAIYYCQQYHHLPFIFGGGTKVDFK 107
 61 RFSGSGSGRDYTFIISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
 107 AA; 11648 MW; ACF9B1253ACA1E5D CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.9 kDa protein.
Mus musculus (Mouse).
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1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
 MEDLINE-20183931; Pubmde-10706531;
Shinohara N., Demura T., Fukuda H.;
Isolation of a vascular cell wall-specific monoclonal antibody
recognizing a cell polarity by using a phage display subtraction
method.";
 Myosin-reactive autoantibodies in rheumatic carditis and normal
 60.1%; Score 337.5; DB 11; Length 298; 58.9%; Pred. No. 3.9e-30; Live 19; Mismatches 24; Indels 1;
 59.9%; Score 336.5; DB 4; Length 108; 60.2%; Pred. No. 1.5e-30; Live 17; Mismatches 23; Indels 3;
 MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
 01-MAY-2000 (TIEWBLrel. 13, Created)
01-MAY-2000 (TIEWBLrel. 13, Last sequence update)
01-DEC-2001 (TIEWBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
 RFSGSGGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGGGTKVEIK 106
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK 106
 233 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK 279
 298 AA; 31867 MW; E0F96B8A17004317 CRC64;
 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;
 Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
EMBL; AB036341; BAA88633.1; -.
HSSP; P01607; IREI.
 Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035031; AAD56267.1; -.
HSSP; P80362; 1WTL.
 PRT;
 TISSUE-SPLEEN;
 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
 Best Local Similarity 58.9%
Matches 63; Conservative
 Conservative
 PRELIMINARY;
 Pfam; PF00047; 19; 2.
SMART; SM00406; IGv; 2.
 SEQUENCE FROM N.A.
 Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID-9606;
 STRAIN-BALB/C;
 65;
 (Fragment).
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 21 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQRPDGTVKLLIYYTSRLYLGVPS 80
 1 DIOMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
 Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.; "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells.";
 Gaps
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 CN 8 SCFV.
CN 8.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 1;
 DB 11; Length 234;
 62.9%; Score 353.5; DB 11; Length 109; 61.7%; Pred. No. 1.8e-32; Live 16; Mismatches 24; Indels 1;
 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Pterin-mimicking anti-idiotope kappa chain variable region
 Query Match 63.3%; Score 355.5; DB 11; Length Best Local Similarity 64.5%; Pred. No. 2.7e-32; Matches 69; Conservative 17; Mismatches 20; Indels
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015292, AAH15292.1; -
InterPro; IPR001806; Ig_MHC.
InterPro; IPR001865; Ribosomal_S2.
PROMITE, PS002091; IG_MHC; UNKNOWN_1.
PROSITE; PS002091; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK 106
 61 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPWTFGGGTKLEIK 107
 Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF307938; AAL09422.1; -.
InterPro, IPR003006; Ig_MHC.
 109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;
 Created)
Last sequence update)
Last annotation update)
 109 AA
 298 AA.
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sed
 PRT;
 PRT;
 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
 66; Conservative
 PRELIMINARY;
 PRELIMINARY;
 109
 Pfam; PF00047; ig; 1.
 Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 (Fragment)
 SEQUENCE
 Query Match
 Best Local
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Q9QYF0;
 RESULT 13
 RESULT 14
 Q9QYF0
 Q920E6
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61 RFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNN-WPFTFGPGTKVDIK 107

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